

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 14:47:14 ; Search time 153 Seconds
(without alignments)
2203.281 Million cell updates/sec

Title: US-10-781-294-24
Perfect score: 5472
Sequence: 1 MLRTAGDGLCRSLTYLEEL.....MTHSLAALRVTRPYLDIGC 1035

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5472	100.0	1035	10	US-09-965-621-24 Sequence 24, Appl
2	5472	100.0	1035	15	US-10-407-866-24 Sequence 24, Appl
3	5472	100.0	1035	16	US-10-781-294-24 Sequence 24, Appl
4	5433	99.3	1061	14	US-10-124-498-18 Sequence 18, Appl
5	5433	99.3	1061	14	US-10-124-498-18 Sequence 18, Appl
6	5259.5	96.1	1027	15	US-10-407-866-68 Sequence 68, Appl
7	5077.5	92.8	1004	15	US-10-108-260A-3161 Sequence 3161, Ap
8	3364	61.5	635	15	US-10-407-866-90 Sequence 90, Appl
9	3163	57.8	603	10	US-09-965-621-64 Sequence 64, Appl
10	3163	57.8	603	15	US-10-407-866-64 Sequence 64, Appl
11	3163	57.8	603	16	US-10-781-294-64 Sequence 22, Appl
12	3005	54.9	582	15	US-10-162-335-22 Sequence 22, Appl
13	2953.5	54.0	565	16	US-10-467-397-9 Sequence 9, Appli

14	2694.5	49.2	521	15	US-10-162-335-24 Sequence 24, Appl
15	2396	43.8	1034	13	US-10-127-516-5 Sequence 5, Appli
16	2396	43.8	1034	13	US-10-027-629-5 Sequence 5, Appli
17	2396	43.8	1034	14	US-10-028-374-18 Sequence 18, Appl
18	2396	43.8	1034	14	US-10-132-967-5 Sequence 5, Appli
19	2396	43.8	1034	14	US-10-183-770-18 Sequence 18, Appl
20	2396	43.8	1034	15	US-10-264-958B-22 Sequence 22, Appl
21	2334	42.7	449	14	US-10-028-374-2 Sequence 2, Appli
22	2334	42.7	449	14	US-10-183-770-2 Sequence 2, Appli
23	1749	32.0	674	15	US-10-407-866-89 Sequence 89, Appl
24	1731	31.6	321	15	US-10-407-866-116 Sequence 116, App
25	1664	30.4	344	9	US-09-799-983-2 Sequence 2, Appli
26	1653.5	30.2	719	10	US-09-965-621-59 Sequence 59, Appl
27	1653.5	30.2	719	15	US-10-407-866-59 Sequence 59, Appl
28	1653.5	30.2	719	16	US-10-781-294-59 Sequence 88, Appl
29	1631.5	29.8	612	15	US-10-407-866-88 Sequence 88, Appl
30	1598	29.2	924	15	US-10-357-820-52 Sequence 52, Appl
31	1457.5	26.6	994	10	US-09-965-621-16 Sequence 16, Appl
32	1457.5	26.6	994	14	US-10-124-498-24 Sequence 24, Appl
33	1457.5	26.6	994	14	US-10-066-521-24 Sequence 24, Appl
34	1457.5	26.6	994	15	US-10-407-866-16 Sequence 16, Appl
35	1457.5	26.6	994	16	US-10-781-294-16 Sequence 16, Appl
36	1456.5	26.6	920	16	US-10-250-615-13 Sequence 13, Appl
37	1432.5	26.2	896	14	US-10-124-498-22 Sequence 22, Appl
38	1432.5	26.2	896	14	US-10-066-521-22 Sequence 22, Appl
39	1385	25.3	1473	15	US-10-182-822A-8 Sequence 8, Appli
40	1381	25.2	1429	14	US-10-029-347-3 Sequence 3, Appli
41	1381	25.2	1429	14	US-10-028-374-3 Sequence 3, Appli
42	1381	25.2	1429	14	US-10-183-770-3 Sequence 3, Appli
43	1375	25.1	1429	9	US-09-996-617-2 Sequence 2, Appli
44	1375	25.1	1429	9	US-09-931-071-2 Sequence 2, Appli
45	1375	25.1	1429	14	US-10-029-347-26 Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-965-621-24
; Sequence 24, Application US/09965621
; Publication NO. US20030077699A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/09/965,621
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-965-621-24

Query Match 100.0%; Score 5472; DB 10; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLRTAGDGLCRSLTYLEELAEVLEKFKLYLGTATELGEGKIPWGSMEKAGPLEMAQLL 60
Db 1 MLRTAGDGLCRSLTYLEELAEVLEKFKLYLGTATELGEGKIPWGSMEKAGPLEMAQLL 60
Qy 61 ITHFGPEAWRLALSTFERINRKDLWERGQEDLVDPQETRYDYVRKFLMEDRNARL 120

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121 ITHFGPEEAWRLALSTFFERINRDLWERGQREDLVDPQETVYVRRKFRMLMEDNARL 120
121 GECVNLSHRYTRLLLVKHSNPMQVQQLDTRGHARTVGHQASPIKTIETLFEDEBRP 180
121 GECVNLSHRYTRLLLVKHSNPMQVQQLDTRGHARTVGHQASPIKTIETLFEDEBRP 180
181 EPRTVMQGAAGIGKSLAHKVMYLDWADGKLPQGRFDYLYFYINCRMNQSAATESMODL 240
181 EPRTVMQGAAGIGKSLAHKVMYLDWADGKLPQGRFDYLYFYINCRMNQSAATESMODL 240
241 IFCWPEPSAPLOELIRVPERLLFIIDGDELKPSFHDPOGWPCLCWEKRPTELLNLSL 300
241 IFCWPEPSAPLOELIRVPERLLFIIDGDELKPSFHDPOGWPCLCWEKRPTELLNLSL 300
301 IRKLLPELSLITTRPTALEKHLRLLHPRHVEILGFSEAEKKEYFYFHNAAEQGV 360
301 IRKLLPELSLITTRPTALEKHLRLLHPRHVEILGFSEAEKKEYFYFHNAAEQGV 360
361 FNYVRDNEPLFTWCFVPLVCWVCTCLOQLEGGLRQTSRTTAVYMLYLLSLMOPKP 420
361 FNYVRDNEPLFTWCFVPLVCWVCTCLOQLEGGLRQTSRTTAVYMLYLLSLMOPKP 420
421 GAPRLQPPNQRGLCSLAADGLWNQKILFEODLRKHGLDGEDVSAFLNWNIFQKDINCE 480
421 GAPRLQPPNQRGLCSLAADGLWNQKILFEODLRKHGLDGEDVSAFLNWNIFQKDINCE 480
481 RYVSFIHLSFQEFPAAMYIILDEGEGAGPDQDVTRLLTEYAFSERSFLATSRFLGLL 540
481 RYVSFIHLSFQEFPAAMYIILDEGEGAGPDQDVTRLLTEYAFSERSFLATSRFLGLL 540
541 NEETRSHLEKSLCWKVSPIKMDLQWIOSKQSDGSTLOQGSLEFSCLEYEQEEFIQ 600
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601 QALSHFOVIVVSNIAKMEHWSVFCIKRCSRSAQVLLHVGATYSADGEDRARCASAGHTL 660
601 QALSHFOVIVVSNIAKMEHWSVFCIKRCSRSAQVLLHVGATYSADGEDRARCASAGHTL 660
661 LVQLRPRTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRGVKKLCOGLRHPNCKLQ 720
661 LVQLRPRTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRGVKKLCOGLRHPNCKLQ 720
721 LRLKRCRISSACEDLSAALTANKNLTRMDLSNGVGFPGMMLLCEGLRHPQCRLOMIQL 780
721 LRLKRCRISSACEDLSAALTANKNLTRMDLSNGVGFPGMMLLCEGLRHPQCRLOMIQL 780

RESULT 2
US-10-407-866-24
; Sequence 24, Application US/10407866
; Publication No. US2004002593A1
; GENERAL INFORMATION:

APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
FILE REFERENCE: 66654-10 (LJ 5755)
CURRENT APPLICATION NUMBER: US/10/407,866
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/370,538
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 1035
TYPE: PRT
ORGANISM: Homo sapien
US-10-407-866-24

Query Match 100.0%; Score 5472; DB 15; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRTAGRDGLCRSLTYLSELEAVALKFKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
Db 1 MLRTAGRDGLCRSLTYLSELEAVALKFKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
QY 61 ITHFGPEEAWRLALSTFFERINRDLWERGQREDLVDPQETVYVRRKFRMLMEDNARL 120
Db 61 ITHFGPEEAWRLALSTFFERINRDLWERGQREDLVDPQETVYVRRKFRMLMEDNARL 120
QY 121 GECVNLSHRYTRLLLVKHSNPMQVQQLDTRGHARTVGHQASPIKTIETLFEDEBRP 180
Db 121 GECVNLSHRYTRLLLVKHSNPMQVQQLDTRGHARTVGHQASPIKTIETLFEDEBRP 180
QY 181 EPRTVMQGAAGIGKSLAHKVMYLDWADGKLPQGRFDYLYFYINCRMNQSAATESMODL 240
Db 181 EPRTVMQGAAGIGKSLAHKVMYLDWADGKLPQGRFDYLYFYINCRMNQSAATESMODL 240
QY 241 IFCWPEPSAPLOELIRVPERLLFIIDGDELKPSFHDPOGWPCLCWEKRPTELLNLSL 300
Db 241 IFCWPEPSAPLOELIRVPERLLFIIDGDELKPSFHDPOGWPCLCWEKRPTELLNLSL 300
QY 301 IRKLLPELSLITTRPTALEKHLRLLHPRHVEILGFSEAEKKEYFYFHNAAEQGV 360
Db 301 IRKLLPELSLITTRPTALEKHLRLLHPRHVEILGFSEAEKKEYFYFHNAAEQGV 360
QY 361 FNYVRDNEPLFTWCFVPLVCWVCTCLOQLEGGLRQTSRTTAVYMLYLLSLMOPKP 420
Db 361 FNYVRDNEPLFTWCFVPLVCWVCTCLOQLEGGLRQTSRTTAVYMLYLLSLMOPKP 420
QY 421 GAPRLQPPNQRGLCSLAADGLWNQKILFEODLRKHGLDGEDVSAFLNWNIFQKDINCE 480
Db 421 GAPRLQPPNQRGLCSLAADGLWNQKILFEODLRKHGLDGEDVSAFLNWNIFQKDINCE 480
QY 481 RYVSFIHLSFQEFPAAMYIILDEGEGAGPDQDVTRLLTEYAFSERSFLATSRFLGLL 540
Db 481 RYVSFIHLSFQEFPAAMYIILDEGEGAGPDQDVTRLLTEYAFSERSFLATSRFLGLL 540
QY 541 NEETRSHLEKSLCWKVSPIKMDLQWIOSKQSDGSTLOQGSLEFSCLEYEQEEFIQ 600
Db 541 NEETRSHLEKSLCWKVSPIKMDLQWIOSKQSDGSTLOQGSLEFSCLEYEQEEFIQ 600
QY 601 QALSHFOVIVVSNIAKMEHWSVFCIKRCSRSAQVLLHVGATYSADGEDRARCASAGHTL 660
Db 601 QALSHFOVIVVSNIAKMEHWSVFCIKRCSRSAQVLLHVGATYSADGEDRARCASAGHTL 660
QY 661 LVQLRPRTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRGVKKLCOGLRHPNCKLQ 720
Db 661 LVQLRPRTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRGVKKLCOGLRHPNCKLQ 720
QY 721 LRLKRCRISSACEDLSAALTANKNLTRMDLSNGVGFPGMMLLCEGLRHPQCRLOMIQL 780
Db 721 LRLKRCRISSACEDLSAALTANKNLTRMDLSNGVGFPGMMLLCEGLRHPQCRLOMIQL 780

Qy 781 RKQLESGACQEMASVLGTNPHLVLDLTGNALBDLGTNLALDGLRLLCQGLRHPVCRRLTLWLKIC 840
Db 781 RKQLESGACQEMASVLGTNPHLVLDLTGNALBDLGTNLALDGLRLLCQGLRHPVCRRLTLWLKIC 840
Qy 841 RLTAACDELASTLSVNSQSLRELDLSNELDGLGVLLLCGLRHPTCKLQTLRLGICRLG 900
Db 841 RLTAACDELASTLSVNSQSLRELDLSNELDGLGVLLLCGLRHPTCKLQTLRLGICRLG 900
Qy 901 SAACEGLSVVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGLTAKA 960
Db 901 SAACEGLSVVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGLTAKA 960
Qy 961 CENLYFTLGINQTLTDLVLTNNALGDTGVRLLCRLSHPGCKLRVLMFGMDLNKMTSHR 1020
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Db 1021 LAALRVTKPYLDIGC 1035
RESULT 3
US-10-781-294-24
; Sequence 24, Application US/10781294
; Publication No. US20040142374A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
; TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/10781,294
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-781-294-24
Query Match 100.0%; Score 5472; DB 16; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLRTAGRDGLCRSLTYLEELAEVLEKPKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
Db 1 MLRTAGRDGLCRSLTYLEELAEVLEKPKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
Qy 61 ITHFGPEAWFLALSTFERINRDKLWERGQEDLVDPQETRYDYVRKFLMEDRNARL 120
Db 61 ITHFGPEAWFLALSTFERINRDKLWERGQEDLVDPQETRYDYVRKFLMEDRNARL 120
Qy 121 GECVNLSHRYTRLLLVKEHSPMVQOQLDGTGRGHARTVGHQASPIKTIETLPDPDEEP 180
Db 121 GECVNLSHRYTRLLLVKEHSPMVQOQLDGTGRGHARTVGHQASPIKTIETLPDPDEEP 180
Qy 181 EPPRTVVMQGAAGIGKSLAHKVMLDWADGKLFQGRFDYLYINCREMNQSAECSCMDL 240
Db 181 EPPRTVVMQGAAGIGKSLAHKVMLDWADGKLFQGRFDYLYINCREMNQSAECSCMDL 240
Qy 241 IFSCWPEPSAPLQELIRVPERLLFIIDGFDLKPSPHDQPGWCLCWEKRPTELLNSL 300
Db 241 IFSCWPEPSAPLQELIRVPERLLFIIDGFDLKPSPHDQPGWCLCWEKRPTELLNSL 300

Qy 301 IRKLLPELSILLITRPTALEKHLRLLEHPRHVEILGFSEARKEYFYKYFHNAEQAOV 360
Db 301 IRKLLPELSILLITRPTALEKHLRLLEHPRHVEILGFSEARKEYFYKYFHNAEQAOV 360
Qy 361 FNYVRDNEPLFTMCFVPLVCMVCTCLOQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKP 420
Db 361 FNYVRDNEPLFTMCFVPLVCMVCTCLOQLEGGGLLRQTSRTTTAVYMLYLLSLMQPKP 420
Qy 421 GAPRLQPPNQRGLCSLAADGLMNOKILFSEODLRKHGLDGEDVSALNNMIFOKDINCE 480
Db 421 GAPRLQPPNQRGLCSLAADGLMNOKILFSEODLRKHGLDGEDVSALNNMIFOKDINCE 480
Qy 481 RYYSFIHLSFQEPFAAMYIILDEGEAGAGPDQDVRTLLTEYAFSERSFLALTTSRFLGGL 540
Db 481 RYYSFIHLSFQEPFAAMYIILDEGEAGAGPDQDVRTLLTEYAFSERSFLALTTSRFLGGL 540
Qy 541 NEETRSHLEKSLCWKVSFPHIKMDLLOWIQSKAQSDGSTLOQGSLEFFSCLYEIEEERFIQ 600
Db 541 NEETRSHLEKSLCWKVSFPHIKMDLLOWIQSKAQSDGSTLOQGSLEFFSCLYEIEEERFIQ 600
Qy 601 QALSHFOVIVVSNIASKMEHVMVSSFCCLKRCSAOLVHLGYATYSADGEDRARCAGAHTL 660
Db 601 QALSHFOVIVVSNIASKMEHVMVSSFCCLKRCSAOLVHLGYATYSADGEDRARCAGAHTL 660
Qy 661 LVQLRPERTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRGVKKLCCQGLRHPNCKLQN 720
Db 661 LVQLRPERTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRGVKKLCCQGLRHPNCKLQN 720
Qy 721 LRLKRCRISSACEDLSAALIANKLTRMDLSGNGVFPGMMLLCEGLRHPQCRLOMTQL 780
Db 721 LRLKRCRISSACEDLSAALIANKLTRMDLSGNGVFPGMMLLCEGLRHPQCRLOMTQL 780
Qy 781 RKQLESGACQEMASVLGTNPHLVLDLTGNALBDLGTNLALDGLRLLCQGLRHPVCRRLTLWLKIC 840
Db 781 RKQLESGACQEMASVLGTNPHLVLDLTGNALBDLGTNLALDGLRLLCQGLRHPVCRRLTLWLKIC 840
Qy 841 RLTAACDELASTLSVNSQSLRELDLSNELDGLGVLLLCGLRHPTCKLQTLRLGICRLG 900
Db 841 RLTAACDELASTLSVNSQSLRELDLSNELDGLGVLLLCGLRHPTCKLQTLRLGICRLG 900
Qy 901 SAACEGLSVVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGLTAKA 960
Db 901 SAACEGLSVVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGLTAKA 960
Qy 961 CENLYFTLGINQTLTDLVLTNNALGDTGVRLLCRLSHPGCKLRVLMFGMDLNKMTSHR 1020
Db 961 CENLYFTLGINQTLTDLVLTNNALGDTGVRLLCRLSHPGCKLRVLMFGMDLNKMTSHR 1020
Qy 1021 LAALRVTKPYLDIGC 1035
Db 1021 LAALRVTKPYLDIGC 1035
RESULT 4
US-10-124-498-18
; Sequence 18, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31

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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-124-498-18

Query Match      99.3%; Score 5433; DB 14; Length 1061;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1034; Conservative 0; Mismatches 0; Indels 28; Gaps 2;

QY 1 MLRTAGDGLCRSLTYLEAEVLEAVELKFKLYLTATLGEGLKIPWGSMEKAGLEMAQLL 60
DB 1 MLRTAGDGLCRSLTYLEAEVLEAVELKFKLYLTATLGEGLKIPWGSMEKAGLEMAQLL 60
QY 61 ITHFGPEAWRLALSTPERINRKLWERGQREDLVR----- 96
DB 61 ITHFGPEAWRLALSTPERINRKLWERGQREDLVR----- 96
QY 97 ---DPOETRYDYVRKFRMLMEDNARLGEVCNLSHRYTRILLVKEHSNPMQVQQLDGTG 153
DB 121 PRKDPQETRYDYVRKFRMLMEDNARLGEVCNLSHRYTRILLVKEHSNPMQVQQLDGTG 180
QY 154 RGHARTVGHQASPIKIEITLPEPDEERPEPPRTVVMQGAAGIGKSMIAHKVMDWADGKLF 213
DB 181 RGHARTVGHQASPIKIEITLPEPDEERPEPPRTVVMQGAAGIGKSMIAHKVMDWADGKLF 240
QY 214 QGRFDYLYNCREMNSQATECSMDLIIFSCWPEPSAPLOELIRVPERLLFIIDGDELK 273
DB 241 QGRFDYLYNCREMNSQATECSMDLIIFSCWPEPSAPLOELIRVPERLLFIIDGDELK 300
QY 274 PSFHDPPQPCWLCWEERKPTPELLNSLIRKLLPELSLITTRPTALEKHLRLEHPRHV 333
DB 301 PSFHDPPQPCWLCWEERKPTPELLNSLIRKLLPELSLITTRPTALEKHLRLEHPRHV 360
QY 334 EILGFSAEARKEYFYKYFHNAEQAGQVFNVRDNEPLFTWCFLVVCWVCTCLOOQLEG 393
DB 361 EILGFSAEARKEYFYKYFHNAEQAGQVFNVRDNEPLFTWCFLVVCWVCTCLOOQLEG 420
QY 394 GGLLRQTSRTTAVYMLYLLSLMQPKGAPRLQPPNQRGLCSLAADGLWNQKILFEEQD 453
DB 421 GGLLRQTSRTTAVYMLYLLSLMQPKGAPRLQPPNQRGLCSLAADGLWNQKILFEEQD 480
QY 454 LRKHGLDGEDVSFAFLNMIFQKIDNCERYYSFIHLSFOEFAAMYIILDEGGAGDQD 513
DB 481 LRKHGLDGEDVSFAFLNMIFQKIDNCERYYSFIHLSFOEFAAMYIILDEGGAGDQD 540
QY 514 VTRLLTEYAFSERSFALTSRFLGLLNEETRSKLSLWKVSPHISKWDLLOWIQSKAQ 573
DB 541 VTRLLTEYAFSERSFALTSRFLGLLNEETRSKLSLWKVSPHISKWDLLOWIQSKAQ 600
QY 574 SDGSTLQOGLSLEFFSCLYEIQEEFTQOALSHPFVIVVSNVSNVSNVSNVSNVSNVSNV 633
DB 601 SDGSTLQOGLSLEFFSCLYEIQEEFTQOALSHPFVIVVSNVSNVSNVSNVSNVSNVSNV 660
QY 634 QVHLHYGATYSADGEDRACSGAHTLVOLPERTVLLDAYSEHLAALCTNPNLIELS 693
DB 661 QVHLHYGATYSADGEDRACSGAHTLVOLPERTVLLDAYSEHLAALCTNPNLIELS 719
QY 694 LYRNALGSRGVKLLCCOGLRHPNCKLQNLRLKRCRISACEDLSAALIANKNLTMDLSG 753
DB 720 LYRNALGSRGVKLLCCOGLRHPNCKLQNLRLKRCRISACEDLSAALIANKNLTMDLSG 779
QY 754 NGVGFPGMMLLCGLRHPQRLQMIQIRKCOLESAGACQEMASVILCTNPHLVELDITGNAL 813
DB 780 NGVGFPGMMLLCGLRHPQRLQMIQIRKCOLESAGACQEMASVILCTNPHLVELDITGNAL 839
QY 814 EDLGLRLCCOGLRHPVCRLLTLMKICRLTAACDELASTLSVNOQSRELDLSLNEGLDL 873
DB 840 EDLGLRLCCOGLRHPVCRLLTLMKICRLTAACDELASTLSVNOQSRELDLSLNEGLDL 899
QY 874 GVLLLCGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRLRELDLSFNDLGDWGLW 933

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DB 900 GVLLLCGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRLRELDLSFNDLGDWGLW 959
QY 934 LLAEGLOHPACRLQKWLMDSCGLTAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC 993
DB 960 LLAEGLOHPACRLQKWLMDSCGLTAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC 1019
QY 994 KRLSHRCKLRLVWLFGMDLNKMTSHSLAALRVTKPYLDIGC 1035
DB 1020 KRLSHRCKLRLVWLFGMDLNKMTSHSLAALRVTKPYLDIGC 1061

RESULT 5
US-10-066-521-18
; Sequence 18, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1061
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-066-521-18

Query Match      99.3%; Score 5433; DB 14; Length 1061;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1034; Conservative 0; Mismatches 0; Indels 28; Gaps 2;

QY 1 MLRTAGDGLCRSLTYLEAEVLEAVELKFKLYLTATLGEGLKIPWGSMEKAGLEMAQLL 60
DB 1 MLRTAGDGLCRSLTYLEAEVLEAVELKFKLYLTATLGEGLKIPWGSMEKAGLEMAQLL 60
QY 61 ITHFGPEAWRLALSTPERINRKLWERGQREDLVR----- 96
DB 61 ITHFGPEAWRLALSTPERINRKLWERGQREDLVR----- 96
QY 97 ---DPOETRYDYVRKFRMLMEDNARLGEVCNLSHRYTRILLVKEHSNPMQVQQLDGTG 153
DB 121 PRKDPQETRYDYVRKFRMLMEDNARLGEVCNLSHRYTRILLVKEHSNPMQVQQLDGTG 180
QY 154 RGHARTVGHQASPIKIEITLPEPDEERPEPPRTVVMQGAAGIGKSMIAHKVMDWADGKLF 213
DB 181 RGHARTVGHQASPIKIEITLPEPDEERPEPPRTVVMQGAAGIGKSMIAHKVMDWADGKLF 240
QY 214 QGRFDYLYNCREMNSQATECSMDLIIFSCWPEPSAPLOELIRVPERLLFIIDGDELK 273
DB 241 QGRFDYLYNCREMNSQATECSMDLIIFSCWPEPSAPLOELIRVPERLLFIIDGDELK 300
QY 274 PSFHDPPQPCWLCWEERKPTPELLNSLIRKLLPELSLITTRPTALEKHLRLEHPRHV 333
DB 301 PSFHDPPQPCWLCWEERKPTPELLNSLIRKLLPELSLITTRPTALEKHLRLEHPRHV 360
QY 334 EILGFSAEARKEYFYKYFHNAEQAGQVFNVRDNEPLFTWCFLVVCWVCTCLOOQLEG 393
DB 361 EILGFSAEARKEYFYKYFHNAEQAGQVFNVRDNEPLFTWCFLVVCWVCTCLOOQLEG 420
QY 394 GGLLRQTSRTTAVYMLYLLSLMQPKGAPRLQPPNQRGLCSLAADGLWNQKILFEEQD 453
DB 421 GGLLRQTSRTTAVYMLYLLSLMQPKGAPRLQPPNQRGLCSLAADGLWNQKILFEEQD 480

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QY 454 LRKHGLEDGEDVSFAFLNNMIFOKDINCERYYSFIHLSFOEFFFAAMYIILDEGEGAGDPD 513
Db 481 LRKHGLEDGEDVSFAFLNNMIFOKDINCERYYSFIHLSFOEFFFAAMYIILDEGEGAGDPD 540
QY 514 VTRLLTEYAFSERSFLATSRFLGLNEETRSHLEKSLCWKSPHIKMDLLOWIQSKAQ 573
Db 541 VTRLLTEYAFSERSFLATSRFLGLNEETRSHLEKSLCWKSPHIKMDLLOWIQSKAQ 600
QY 574 SDGSTLOQGSLEFFSCLYEIOEEFIOQALSHFQIVVSNIASKMEHVMVSFCLKRCRSA 633
Db 601 SDGSTLOQGSLEFFSCLYEIOEEFIOQALSHFQIVVSNIASKMEHVMVSFCLKRCRSA 660
QY 634 QVLHLYGATYSADGEDRARCAGAHNTLLVQLRPRTVLLDAYSEHAAALCTNPNLIELS 693
Db 661 QVLHLYGATYSADGEDRARCAGAHNTLLVQLRPRTVLLDAYSEHAAALCTNPNLIELS 719
QY 694 LYRNALGSRGVKLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 753
Db 720 LYRNALGSRGVKLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 779
QY 754 NGVFPFGMWLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 813
Db 780 NGVFPFGMWLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 839
QY 814 EDGLRLCCOGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 873
Db 840 EDGLRLCCOGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 899
QY 874 GVLLCEGLRHPTCKLQTLRGI CRLGSAACEGLSVVLQANHNRELDLSFNDLGDWGLW 933
Db 900 GVLLCEGLRHPTCKLQTLRGI CRLGSAACEGLSVVLQANHNRELDLSFNDLGDWGLW 959
QY 934 LLAEGLOHPACRLQKLLDSCGLTAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC 993
Db 960 LLAEGLOHPACRLQKLLDSCGLTAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC 1019
QY 994 KRLSHPGKLVLMFGMDLNKMTSHRLAALRVTKPYLDIGC 1035
Db 1020 KRLSHPGKLVLMFGMDLNKMTSHRLAALRVTKPYLDIGC 1061

RESULT 6
US-10-407-866-68
; Sequence 68, Application US/10407866
; Publication No. US20040002593A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
; FILE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: 66654-10 (LJ 5755)
; CURRENT APPLICATION NUMBER: US/10/407,866
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,538
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-407-866-68

Query Match 96.1%; Score 5259.5; DB 15; Length 1027;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 MLRTAGRDGLCRSLTYLBEAVALKKFKLYLGATLGECKIPWGSMEKAGPLEMAQLL 60
Db 1 MLRTAGRDGLCRSLTYLBEAVALKKFKLYLGATLGECKIPWGSMEKAGPLEMAQLL 60
QY 61 ITHFGPEAWRLALSTFERINRKDLWERGQREDLVR----- 96
|||||
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Db 61 ITHFGPEAWRLALSTFERINRKDLWERGQREDLVRDTPPGPSSLSGNQSTCLLEVSIVT 120
QY 97 ---DPQETRYDYVRKFRLEMDRNARLGEVCYNLSHRVYTRLLLVKHSNPMVQOQLDGTG 153
Db 121 PRKDPQETRYDYVRKFRLEMDRNARLGEVCYNLSHRVYTRLLLVKHSNPMVQOQLDGTG 180
QY 154 RGHARTVGHQASPIKIEITLPEPDEBERPPRTVVMQGAAGIGKSMLAHKVMDWADGKLF 213
Db 181 RGHARTVGHQASPIKIEITLPEPDEBERPPRTVVMQGAAGIGKSMLAHKVMDWADGKLF 240
QY 214 QGRFDYLPYINCREMNOSATECSMODLIFSCWPSAPLOELIRVPERLLFIIDGFDLKL 273
Db 241 QGRFDYLPYINCREMNOSATECSMODLIFSCWPSAPLOELIRVPERLLFIIDGFDLKL 300
QY 274 PSFHDPOGPWCLCWEKRPTELLNLSLRKLLPELSLITRTPALEKHLRLEHPRHV 333
Db 301 PSFHDPOGPWCLCWEKRPTELLNLSLRKLLPELSLITRTPALEKHLRLEHPRHV 360
QY 334 EILGFSAEARKEYFYKTFHNAEQAGQVFNVRDNEPLFTMCFVPLVVCWVCTCLOOQLEG 393
Db 361 EILGFSAEARKEYFYKTFHNAEQAGQVFNVRDNEPLFTMCFVPLVVCWVCTCLOOQLEG 420
QY 394 GGLLRQTSRTTTAVYMLYLLSLMQPKCAPLQPPNQRGKLSLAADGLWNQKILFEQD 453
Db 421 GGLLRQTSRTTTAVYMLYLLSLMQPKCAPLQPPNQRGKLSLAADGLWNQKILFEQD 480
QY 454 LRKHGLEDGEDVSFAFLNNMIFOKDINCERYYSFIHLSFOEFFFAAMYIILDEGEGAGDPD 513
Db 481 LRKHGLEDGEDVSFAFLNNMIFOKDINCERYYSFIHLSFOEFFFAAMYIILDEGEGAGDPD 540
QY 514 VTRLLTEYAFSERSFLATSRFLGLNEETRSHLEKSLCWKSPHIKMDLLOWIQSKAQ 573
Db 541 VTRLLTEYAFSERSFLATSRFLGLNEETRSHLEKSLCWKSPHIKMDLLOWIQSKAQ 600
QY 574 SDGSTLOQGSLEFFSCLYEIOEEFIOQALSHFQIVVSNIASKMEHVMVSFCLKRCRSA 633
Db 601 SDGSTLOQGSLEFFSCLYEIOEEFIOQALSHFQIVVSNIASKMEHVMVSFCLKRCRSA 660
QY 634 QVLHLYGATYSADGEDRARCAGAHNTLLVQLRPRTVLLDAYSEHAAALCTNPNLIELS 693
Db 661 QVLHLYGATYSADGEDRARCAGAHNTLLVQLRPRTVLLDAYSEHAAALCTNPNLIELS 720
QY 694 LYRNALGSRGVKLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 753
Db 721 LYRNALGSRGVKLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 780
QY 754 NGVFPFGMWLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 813
Db 781 NGVFPFGMWLLCEGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 840
QY 814 EDGLRLCCOGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 873
Db 841 EDGLRLCCOGLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSG 900
QY 874 GVLLCEGLRHPTCKLQTLRGI CRLGSAACEGLSVVLQANHNRELDLSFNDLGDWGLW 933
Db 901 GVLLCEGLRHPTCKLQTLRGI CRLGSAACEGLSVVLQANHNRELDLSFNDLGDWGLW 960
QY 934 LLAEGLOHPACRLQKLLDSCGLTAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC 993
Db 961 LLAEGLOHPACRLQKLLDSCGLTAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC 1020
QY 994 KRLSHPG 1000
Db 1021 KRLSHPG 1027

RESULT 7
US-10-108-260A-3161
; Sequence 3161, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
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[illegible]

Qy 481 RYYSFIHLSFQEFFAAMYIILDEGGAGPDQDVTRLLTEYAFSERSFLATSRFLGILL 540
Db |||||
Qy 481 RYYSFIHLSFQEFFAAMYIILDEGGAGPDQDVTRLLTEYAFSERSFLATSRFLGILL 540
Db |||||
Qy 541 NEETRSHLEKSLCWKVSPIHKMDLLQWIOSKQSDGSTLOQGSLEFFSCLYEIOBEETFIQ 600
Db |||||
Qy 541 NEETRSHLEKSLCWKVSPIHKMDLLQWIOSKQSDGSTLOQGSLEFFSCLYEIOBEETFIQ 600
Db |||||
Qy 601 QALSHFQIVVSNIASKMEHVMVSFCLKRCRSAQV 635
Db |||||
Qy 601 QALSHFQIVVSNIASKMEHVMVSFCLKRCRSAQV 635
Db |||||

RESULT 9

US-09-965-621-64
; Sequence 64, Application US/09965621
; Publication No. US20030077699A1
; GENERAL INFORMATION:

; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowaki, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-965-621-64

Query Match 57.8%; Score 3163; DB 10; Length 603;
Best Local Similarity 100.0%; Pred. No. 5.7e-274;
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 PNQGLCSLAADGLWNQKILFEEQDLRKHGIDGEDVSAFLNMNIFQKDINCERYYSFIHL 488
Db 1 PNQGLCSLAADGLWNQKILFEEQDLRKHGIDGEDVSAFLNMNIFQKDINCERYYSFIHL 60
Qy 489 SFQEFFAAMYIILDEGGAGPDQDVTRLLTEYAFSERSFLATSRFLGILLNEETRSHL 548
Db 61 SFQEFFAAMYIILDEGGAGPDQDVTRLLTEYAFSERSFLATSRFLGILLNEETRSHL 120
Qy 549 EKSICWKVSPIHKMDLLQWIOSKQSDGSTLOQGSLEFFSCLYEIOBEETFIQALSHFQV 608
Db 121 EKSICWKVSPIHKMDLLQWIOSKQSDGSTLOQGSLEFFSCLYEIOBEETFIQALSHFQV 180
Qy 609 IIVSNIASKMEHVMVSFCLKRCRSAQVHLHYGATYSADGEDRARCSCAGAHLLVQLRPER 668
Db 181 IIVSNIASKMEHVMVSFCLKRCRSAQVHLHYGATYSADGEDRARCSCAGAHLLVQLRPER 240
Qy 669 TVLLDAYSEHLAAALCTNPNIIELSLYRNALSGRGVLLCCQGRHPNCKLQNLKRCRI 728
Db 241 TVLLDAYSEHLAAALCTNPNIIELSLYRNALSGRGVLLCCQGRHPNCKLQNLKRCRI 300
Qy 729 SSSACEDLSAALIANKNLTMRDLSGNGVGPFGMWLLCEGLRHPQCRQMIOLRKCOLESG 788
Db 301 SSSACEDLSAALIANKNLTMRDLSGNGVGPFGMWLLCEGLRHPQCRQMIOLRKCOLESG 360
Qy 789 ACQEMASVLGTNPHLVELDTGNALDGLRLCCQGRHPVCRRLTLWLKICRLTAACD 848
Db 361 ACQEMASVLGTNPHLVELDTGNALDGLRLCCQGRHPVCRRLTLWLKICRLTAACD 420

Qy 849 ELASTLSVNSQSLRELDLSLNELDGLVLLLCCEGLRHPCTKQLQTLRLGICRLGSAACEGLS 908
Db |||||
Qy 421 ELASTLSVNSQSLRELDLSLNELDGLVLLLCCEGLRHPCTKQLQTLRLGICRLGSAACEGLS 480
Db |||||
Qy 909 VVLQANHNRLDLSFNDLGDWGLWLAEGLOHPACRLQKWLDSGGLTAKACENLYFTL 968
Db |||||
Qy 481 VVLQANHNRLDLSFNDLGDWGLWLAEGLOHPACRLQKWLDSGGLTAKACENLYFTL 540
Db |||||
Qy 969 GINQTLTDLVLTNNALGDTGVRLLCCKRLSHPGCKRLVILWLFMDLNKMTSHRLAALRVTK 1028
Db |||||
Qy 541 GINQTLTDLVLTNNALGDTGVRLLCCKRLSHPGCKRLVILWLFMDLNKMTSHRLAALRVTK 600
Db |||||
Qy 1029 PYL 1031
Db |||||
Qy 601 PYL 603
Db |||||

RESULT 10

US-10-407-866-64
; Sequence 64, Application US/10407866
; Publication No. US20040002593A1
; GENERAL INFORMATION:

; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
; FILE REFERENCE: 66654-10(LJ 5755)
; CURRENT APPLICATION NUMBER: US/10/407,866
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,538
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-407-866-64

Query Match 57.8%; Score 3163; DB 15; Length 603;
Best Local Similarity 100.0%; Pred. No. 5.7e-274;
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 PNQGLCSLAADGLWNQKILFEEQDLRKHGIDGEDVSAFLNMNIFQKDINCERYYSFIHL 488
Db 1 PNQGLCSLAADGLWNQKILFEEQDLRKHGIDGEDVSAFLNMNIFQKDINCERYYSFIHL 60
Qy 489 SFQEFFAAMYIILDEGGAGPDQDVTRLLTEYAFSERSFLATSRFLGILLNEETRSHL 548
Db 61 SFQEFFAAMYIILDEGGAGPDQDVTRLLTEYAFSERSFLATSRFLGILLNEETRSHL 120
Qy 549 EKSICWKVSPIHKMDLLQWIOSKQSDGSTLOQGSLEFFSCLYEIOBEETFIQALSHFQV 608
Db 121 EKSICWKVSPIHKMDLLQWIOSKQSDGSTLOQGSLEFFSCLYEIOBEETFIQALSHFQV 180
Qy 609 IIVSNIASKMEHVMVSFCLKRCRSAQVHLHYGATYSADGEDRARCSCAGAHLLVQLRPER 668
Db 181 IIVSNIASKMEHVMVSFCLKRCRSAQVHLHYGATYSADGEDRARCSCAGAHLLVQLRPER 240
Qy 669 TVLLDAYSEHLAAALCTNPNIIELSLYRNALSGRGVLLCCQGRHPNCKLQNLKRCRI 728
Db 241 TVLLDAYSEHLAAALCTNPNIIELSLYRNALSGRGVLLCCQGRHPNCKLQNLKRCRI 300
Qy 729 SSSACEDLSAALIANKNLTMRDLSGNGVGPFGMWLLCEGLRHPQCRQMIOLRKCOLESG 788
Db 301 SSSACEDLSAALIANKNLTMRDLSGNGVGPFGMWLLCEGLRHPQCRQMIOLRKCOLESG 360
Qy 789 ACQEMASVLGTNPHLVELDTGNALDGLRLCCQGRHPVCRRLTLWLKICRLTAACD 848
Db 361 ACQEMASVLGTNPHLVELDTGNALDGLRLCCQGRHPVCRRLTLWLKICRLTAACD 420
Qy 849 ELASTLSVNSQSLRELDLSLNELDGLVLLLCCEGLRHPCTKQLQTLRLGICRLGSAACEGLS 908
Db |||||

Wed Feb 9 10:22:14 2005

Db 421 ELASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPTCKLQTLRLGICRLGSAACEGLS 480
QY 909 VVLQAHNRLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGGLTAKACENLYFTL 968
Db 481 VVLQAHNRLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGGLTAKACENLYFTL 540
QY 969 GINQTLTDLYLTNNALGDTGVRLLCKRLSHPGCKLRVWLFGMDLNKMTSHSLAALRVTK 1028
Db 541 GINQTLTDLYLTNNALGDTGVRLLCKRLSHPGCKLRVWLFGMDLNKMTSHSLAALRVTK 600
QY 1029 PYL 1031
Db 601 PYL 603
RESULT 11
US-10-781-294-64
; Sequence 64, Application US/10781294
; Publication No. US20040142374A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAD Domain-Containing Polypeptides,
; TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/10/781,294
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-781-294-64
Query March 57.8%; Score 3163; DB 16; Length 603;
Best Local Similarity 100.0%; Pred. No. 5.7e-274;
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 429 PNQGLCSLAADGLWNNQKILFEQDLRKHGLDGEDVSFAFLNNIFQKDINCERYYSFIHL 488
Db 1 PNQGLCSLAADGLWNNQKILFEQDLRKHGLDGEDVSFAFLNNIFQKDINCERYYSFIHL 60
QY 489 SFQEFFAAMYIILDEGGGAGPDQVTRLITEYAFSERSFLALTSRFLGLNEETRSHL 548
Db 61 SFQEFFAAMYIILDEGGGAGPDQVTRLITEYAFSERSFLALTSRFLGLNEETRSHL 120
QY 549 EKSLCWKVSPIKMDLLQWTSQAQSDGSTLQGSLEFFSCLYEIOEEFIOQALSHFOV 608
Db 121 EKSLCWKVSPIKMDLLQWTSQAQSDGSTLQGSLEFFSCLYEIOEEFIOQALSHFOV 180
QY 609 IWVSNIAKMEHMYVSFCLKCRSAQVHLGYATYSADGEDRARCAGAHTLVLQRLRP 668
Db 181 IWVSNIAKMEHMYVSFCLKCRSAQVHLGYATYSADGEDRARCAGAHTLVLQRLRP 240
QY 669 TVLLDAYSEHLAAALCTNPNLIELSLRYNALGSGVKLLCQGLRHPCNKLQNLKRCRI 728
Db 241 TVLLDAYSEHLAAALCTNPNLIELSLRYNALGSGVKLLCQGLRHPCNKLQNLKRCRI 300
QY 729 SSSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLCEGLRHPCNKLQNLKRCRI 788
Db 301 SSSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLCEGLRHPCNKLQNLKRCRI 848
QY 789 ACOEMASVLGTNPHLVLDLTGNALEDLGLRLCCGLRHPCNKLQNLKRCRI 848

Db 361 ACOEMASVLGTNPHLVLDLTGNALEDLGLRLCCGLRHPCNKLQNLKRCRI 420
QY 849 ELASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPTCKLQTLRLGICRLGSAACEGLS 908
Db 421 ELASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPTCKLQTLRLGICRLGSAACEGLS 480
QY 909 VVLQAHNRLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGGLTAKACENLYFTL 968
Db 481 VVLQAHNRLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKWLDSGGLTAKACENLYFTL 540
QY 969 GINQTLTDLYLTNNALGDTGVRLLCKRLSHPGCKLRVWLFGMDLNKMTSHSLAALRVTK 1028
Db 541 GINQTLTDLYLTNNALGDTGVRLLCKRLSHPGCKLRVWLFGMDLNKMTSHSLAALRVTK 600
QY 1029 PYL 1031
Db 601 PYL 603
RESULT 12
US-10-162-335-22
; Sequence 22, Application US/10162335
; Publication No. US20040009480A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Boldog, Perenc L.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Hjalt, Tord
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Metho
; FILE REFERENCE: 21402-377 B
; CURRENT APPLICATION NUMBER: US/10/162,335
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883

; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM:
; NUMBER OF SEQ ID NOS: 201
; SEQ ID NO 22
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-22

Query Match 54.9%; Score 3005; DB 15; Length 582;
Best Local Similarity 99.3%; Pred. No. 7.8e-260;
Matches 578; Conservative 0; Mismatches 0; Indels 4; Gaps 3;
Qy 373 MCFPLVCWVCTCLOQLEGGLRQTSRTTAVYMLYLSLMPKPGAPRLQPPNQ 432
Db 1 MCFPLVCWVCTCLOQLEGGLRQTSRTTAVYMLYLSLMPKPGAPRLQPPNQ 60
Qy 433 GLCSLAADGLNOKLFEQDLRKHGLDGEDVSAPLNNIFQKDCINCYRYSFHLSFOE 492
Db 61 GLCSLAADGLNOKLFEQDLRKHGLDGEDVSAPLNNIFQKDCINCYRYSFHLSFOE 120
Qy 493 FFAAMYIILDEGEGAGPDQVTRLLTEYAFSERSFALTSRFLFGLLNEETRSHLEKSL 552
Db 121 FFAAMYIILDEGEGAGPDQVTRLLTEYAFSERSFALTSRFLFGLLNEETRSHLEKSL 180
Qy 553 CWKVSPIKMDLLQWIOSKASDGSSTLQGSLEFPSCLYEIOEBSFIOQALSHPFQVVS 612
Db 181 CWKVSPIKMDLLQWIOSKASDGSSTLQGSLEFPSCLYEIOEBSFIOQALSHPFQVVS 240
Qy 613 NIASKMEHWSFCLKRCRSQVLLHYGATYSADGEDRARSAGAHLLVOLRPERTVLL 672
Db 241 NIASKMEHWSFCLKRCRSQVLLHYGATYSADGEDRARSAGAHLLVOLRPERTVLL 300
Qy 673 DAYSEHLAAALCTPNLIELSLYRNALSGRVKLLCOGLRHPNCKLQNL-RLKRCRISSS 731
Db 301 DAYSEHLAAALCTPNLIELSLYRNALSGRVKLLCOGLRHPNCKLQNLRLKRCRISSS 360
Qy 732 ACEDLSAALIANKNLTRMDLSGNGVGFPGMMLCEGLRHPQCRLOMIQLRKCQLESACQ 791
Db 361 ACEDLSAALIANKNLTRMDLSGNGVGFPGMMLCEGLRHPQCRLOMIQLRKCQLESACQ 420
Qy 792 EMASVGLTNPHVELDTGNALEDGLRLLCQGLRHPVCRRLTW-LKICRLTAACDE 849
Db 421 EMASVGLTNPHVELDTGNALEDGLRLLCQGLRHPVCRRLTWLWCRLLKICRLTAACDE 480
Qy 850 LASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPCTCKLOTL-RLGICRLGSAACEGLS 908
Db 481 LASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPCTCKLOTLRLGICRLGSAACEGLS 540
Qy 909 VVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKLW 950
Db 541 VVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKLW 582

RESULT 13
US-10-467-397-9
; Sequence 9, Application US/10467397
; Publication No. US20040137448A1
; GENERAL INFORMATION:
; APPLICANT: THORNTON, Michael; HAFALIA, April J.A.;
; APPLICANT: LU, Dyung Aina M.; ARVIZU, Chandra S.;
; APPLICANT: SWARNAKAR, Anita; LU, Yan;
; APPLICANT: WARREN, Bridget A.; BAUGHN, Mariah R.;
; APPLICANT: TANG, Y. Tom; LEE, Ernestine A.;
; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;
; APPLICANT: KHAN, Farrah A.; GANDHI, Ameena R.;
; APPLICANT: DING, Li; YUE, Henry;
; APPLICANT: GIETZEN, Kimberly J.; CHAWLA, Narinder K.;
; APPLICANT: THANGAVELU, Kavitha; ELLIOTT, Vicki S.
; TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS
; FILE REFERENCE: PI-0368 USN
; CURRENT APPLICATION NUMBER: US/10/467,397

; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03844
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/268,118
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/270,963
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,858
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/271,194
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,071
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/283,496
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/344,650
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 429930CD1
US-10-467-397-9

Query Match 54.0%; Score 2953.5; DB 16; Length 565;
Best Local Similarity 99.8%; Pred. No. 3.1e-255;
Matches 565; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 470 MNIFQKDCINCYRYSFHLSFOEFAAMYIILDEGEGAGPDQVTRLLTEYAFSERSFL 529
Db 1 MNIFQKDCINCYRYSFHLSFOEFAAMYIILDEGEGAGPDQVTRLLTEYAFSERSFL 60
Qy 530 ALTSRFLFGLLNEETRSHLEKSLCWKVSPIKMDLLQWIOSKASDGSSTLQGSLEFPSC 589
Db 61 ALTSRFLFGLLNEETRSHLEKSLCWKVSPIKMDLLQWIOSKASDGSSTLQGSLEFPSC 120
Qy 590 LYETOEEFTQOALSHPFQVIVSNIAKMEHWSFCLKRCRSQVLLHYGATYSADGED 649
Db 121 LYETOEEFTQOALSHPFQVIVSNIAKMEHWSFCLKRCRSQVLLHYGATYSADGED 180
Qy 650 RARCSAGAHLLVOLRPERTVLLDAYSEHLAAALCTPNLIELSLYRNALSGRVKLLCQ 709
Db 181 RARCSAGAHLLVOL-PERTVLLDAYSEHLAAALCTPNLIELSLYRNALSGRVKLLCQ 239
Qy 710 GLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLCEGLR 769
Db 240 GLRHPNCKLQNLRLKRCRISSSACEDLSAALIANKNLTRMDLSGNGVGFPGMMLCEGLR 299
Qy 770 HPQCRLOMIQLRKCQLESACQEMASVGLTNPHVELDTGNALEDGLRLLCQGLRHPV 829
Db 300 HPQCRLOMIQLRKCQLESACQEMASVGLTNPHVELDTGNALEDGLRLLCQGLRHPV 359
Qy 830 CRLFTLMLKICRLTAACDELAESTLSVNQSLRELDLSNELGDLGVLLCEGLRHPCTCKL 889
Db 360 CRLFTLMLKICRLTAACDELAESTLSVNQSLRELDLSNELGDLGVLLCEGLRHPCTCKL 419
Qy 890 QTLRLGICRLGSAACEGLSVVVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKL 949
Db 420 QTLRLGICRLGSAACEGLSVVVLQANHNLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKL 479
Qy 950 WLDSGGLTAKACENLYFTLGINOTLTDLYLTNNALGDTGVLLCKRLSHPCCKLRVLWLF 1009
Db 480 WLDSGGLTAKACENLYFTLGINOTLTDLYLTNNALGDTGVLLCKRLSHPCCKLRVLWLF 539
Qy 1010 GMDLNKMTSHSLAALRVTKPYLDIGC 1035
Db 540 GMDLNKMTSHSLAALRVTKPYLDIGC 565

RESULT 14
US-10-162-335-24
; Sequence 24, Application US/10162335
; Publication No. US2004009480A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Caaman, Stacie J.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Hjal, Tord
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Li, Li
; APPLICANT: Macdougall, John R.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Stone, David J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
; FILE REFERENCE: 21402-377 B
; CURRENT APPLICATION NUMBER: US/10/162,335
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 201
; SEQ ID NO 24
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-335-24

QY 493 FFAAMYILDEGGAGPDQDVTLLTTEYAFSRSFLALTSRFLFGLNNEETSHLEKSL 552
Db 121 FFAAMYILDEGGAGPDQDVTLLTTEYAFSRSFLALTSRFLFGLNNEETSHLEKSL 180
QY 553 CWKVSPIKMDLLQWIOSKQSGSTLQOQSLFFSCFYIEIEEFIOQALSHFQVIVWS 612
Db 181 CWKVSPIKMDLLQWIOSKQSGSTLQOQSLFFSCFYIEIEEFIOQALSHFQVIVWS 240
QY 613 NIASKMEHVSFCLKECRSAQVHLHYGATYSADGEDRARCASAGAHLLVQLRPERIVLL 672
Db 241 NIASKMEHVSFCLKECRSAQVHLHYGATYSADGEDRARCASAGAHLLVQLRPERIVLL 300
QY 673 DAYSEHLAAALCTNPNLIELSYENALGSRGVKLLCQGLRHPNCKLQNLKRCRISSSA 732
Db 301 DAYSEHLAAALCTNPNLIELSYENALGSRGVKLLCQGLRHPNCKLQNLKRCRISSSA 360
QY 733 CEDLSAALIANKNLTMDLSNGVGFPGMMLLCEGLRHPQCRLOMIQLRKQSLSSGACQE 792
Db 361 CEDLSAALIANKNLTMDLSNGVGFPGMMLLCEGLRHPQCRLOMIQLRKQSLSSGACQE 407
QY 793 MASVLGTNPHLVELDLTGNALEDLGLRLCQGLRHPVCRLTLMLKICRLTAAACDELAS 852
Db 408 MASVLGTNPHLVELDLTGNALEDLGLRLCQGLRHPVCRLTLMLKICRLTAAACDELAS 423
QY 853 TILSVNQSLRELDLSLNEGLDGLVLLCEGLRHPCKLQTLRLGICRIGSAACEGLSVVLQ 912
Db 424 TILSVNQSLRELDLSLNEGLDGLVLLCEGLRHPCKLQTLRLGICRIGSAACEGLSVVLQ 483
QY 913 ANHNRLDLSFNDLGDWGLWLLAEGLOHPACRLQKLW 950
Db 484 ANHNRLDLSFNDLGDWGLWLLAEGLOHPACRLQKLW 521

RESULT 15
US-10-127-516-5
; Sequence 5, Application US/10127516
; Publication No. US20020187922A1
; GENERAL INFORMATION:
; APPLICANT: Manji, Gulam A.
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN DOMAIN
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-370001
; CURRENT APPLICATION NUMBER: US/10/127,516
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 10/027,629
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 09/964,955
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/653,901
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 09/506, 067
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-127-516-5

QY 11 CRISTYLEEAEVAVELKKFKLYL-GTATELGEKIPWGSMEKAGPLEMAQLLIHFGPEEA 69
Db 6 CKLARYLEDLEDVDLKKFKWHELDYPPQKGCIPLRQTEKADHVDLATLMIDFNGBEKA 65
QY 70 WRALSTFERINRKLWERCQRED- 93
Db 66 WAMAVWIFAANRRDLYEKAKRDEPKWGSNARVSNPTVCOEDSIEEWNGLLYLSRI 125

Query Match 43.8%; Score 2396; DB 13; Length 1034;
Best Local Similarity 46.1%; Pred. No. 7e-205;
Matches 495; Conservative 175; Mismatches 303; Indels 100; Gaps 10;
QY 373 MCFVPLVCWVCTCLOQLEGGGLRQTSRTTAVVMLYLLSIMQPKGAPLQPPNQ 432
Db 1 MCFVPLVCWVCTCLOQLEGGGLRQTSRTTAVVMLYLLSIMQPKGAPLQPPNQ 60
QY 433 GLCSLAADGLWNOKILFEODLRKHGLEDVSAFLNMNIFQDINCERYYSFIHLSFOE 492
Db 61 GLCSLAADGLWNOKILFEODLRKHGLEDVSAFLNMNIFQDINCERYYSFIHLSFOE 120

Query Match 49.2%; Score 2694.5; DB 15; Length 521;
Best Local Similarity 90.1%; Pred. No. 4.3e-232;
Matches 521; Conservative 0; Mismatches 0; Indels 57; Gaps 1;
QY 373 MCFVPLVCWVCTCLOQLEGGGLRQTSRTTAVVMLYLLSIMQPKGAPLQPPNQ 432
Db 1 MCFVPLVCWVCTCLOQLEGGGLRQTSRTTAVVMLYLLSIMQPKGAPLQPPNQ 60
QY 433 GLCSLAADGLWNOKILFEODLRKHGLEDVSAFLNMNIFQDINCERYYSFIHLSFOE 492
Db 61 GLCSLAADGLWNOKILFEODLRKHGLEDVSAFLNMNIFQDINCERYYSFIHLSFOE 120

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 14:44:08 ; Search time 50 Seconds
(without alignments)
1991.687 Million cell updates/sec

Title: US-10-781-294-24
Perfect score: 5472
Sequence: 1 MLRTAGRDGLCRUSTYLEEL.....MTHSLAALRVTKPYLDIGC 1035
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1314.5	24.0	1192	2 T17255	hypothetical prote
2	1160.5	21.2	1111	2 A59000	mater protein (imp
3	724	13.2	461	2 A31858	ribonuclease-angio
4	717	13.1	456	2 S20597	ribonuclease inhib
5	709	13.0	456	2 A31857	ribonuclease inhib
6	494.5	9.0	483	2 S27880	Nasopressin recept
7	377.5	6.9	1130	2 A48843	MHC class II trans
8	258	4.7	1004	2 T31665	hypothetical prote
9	216.5	4.0	1075	2 T31668	hypothetical prote
10	183.5	3.4	1232	2 A54748	neutrophil apoptosi
11	180	3.3	312	2 B97746	hypothetical prote
12	179.5	3.3	545	2 T52068	RAN GTPase-activat
13	178	3.3	533	2 T52063	T-complex-associat
14	177.5	3.2	506	2 A45841	hypothetical prote
15	172.5	3.2	618	2 T48193	neutrophil apoptosi
16	171	3.1	1447	2 T42628	hypothetical prote
17	170	3.1	568	2 F86291	hypothetical prote
18	169.5	3.1	789	2 T52067	hypothetical prote
19	169.5	3.1	1121	2 T02764	myosin-I binding p
20	162	3.0	631	2 C89243	protein F28C1.3 (i
21	162	3.0	631	2 T21471	hypothetical prote
22	161.5	3.0	589	2 A36983	RNAI homolog fugi
23	160	2.9	998	2 T23427	hypothetical prote
24	158	2.9	535	2 T48102	RAN GTPase activat
25	156.5	2.9	589	2 T52070	RNAI protein homol
26	155	2.8	587	2 JC5300	Ran GTPase activat
27	152.5	2.8	2493	2 A55481	adenylate cyclase
28	152	2.8	1010	2 T36383	probable large ATP
29	142.5	2.6	1253	2 T45787	disease resistance

30	142	2.6	934	2 T05201	hypothetical prote
31	140.5	2.6	1389	2 T13852	gene wheeler prote
32	140	2.6	1039	2 A85096	hypothetical prote
33	139.5	2.5	271	2 D84586	hypothetical prote
34	138	2.5	526	2 C84552	hypothetical prote
35	137.5	2.5	1237	2 A81915	hypothetical prote
36	137.5	2.5	1385	2 T13887	tlr protein - frui
37	136.5	2.5	1286	2 T33476	hypothetical prote
38	135.5	2.5	1066	2 T15864	hypothetical prote
39	135	2.5	592	2 T52139	LRR-containing F-b
40	135	2.5	1217	2 T52348	disease resistance
41	134.5	2.5	906	2 G96621	probable disease r
42	134.5	2.5	957	2 B84547	probable disease r
43	134	2.4	607	2 F96598	protein F20N2.2 (i
44	133	2.4	1110	2 F84547	probable disease r
45	132.5	2.4	907	2 J50176	orphan G protein-c

ALIGNMENTS

RESULT 1

T17255
hypothetical protein DKFZp586O1822.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17255
R:Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A:Reference number: Z18722
A:Accession: T17255
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1192 <KOE>
A:Cross-references: UNIPROT:Q9C000; EMBL:AL117470
A:Experimental source: adult uterus; clone DKFZp586O1822
C:Genetics:
A:Note: DKFZp586O1822.1

Query Match		24.0%	Score 1314.5;	DB 2;	Length 1192;
Best Local Similarity		39.9%	Pred. No. 2.3e-93;		
Matches 32;		Conservative 119;	Mismatches 293;	Indels 75;	Gaps 19;
Qy	133	LLLVKEH---SNPMQVQ--	QLDITGRGHARTVGHQASPIKTIETLFPDEBPPTTV	187	
Db	1	LLLQRPSPQDPLVKESWPDYVEENRGL	-----IEIRDLFGGLDTQE-PRIV	50	
Qy	188	MQGAAGIGKMLAHKVMLDWADGKLFQGRFDYLPYINCREMNSQATCSMODLIFSCWPE	247		
Db	51	LQGAAGIGKSTLARQVKEAMGRGQLYGDRFQHVYFSCRELAQSKV-VSLAELIGKDGTA	109		
Qy	248	PSAPLQELIRVPERLLFIIDGDELKPSFHDPOGPGWCLCWEKEKPTLLNLSLRKLLP	307		
Db	110	TPAPIQLSRPERLLFIIDGDELKPSFHDPOGPGWCLCWEKEKPTLLNLSLRKLLP	169		
Qy	308	ELSLIITRTALEKHLRLEHPRHVEILGFSAERKEYFYKYFHNAEQAGQVNVYVDN	367		
Db	170	EASFLITARTALQNLPSELEQARWVEVLGFSSSRKEYFYRYTDERQAIRAFRLVKS	229		
Qy	368	EPLFTMCFVPLVCWVVTCTLQQLEGGLLRQTSRTTAVVMLYLLSLMQPKGAPRLQP	427		
Db	230	KELWALCLVPWSWNLACTCLMQMKRKLTLSTKTTTLCLHYLAQALQAPLGPQL--	287		
Qy	428	PPNQRGICSLAAGLNNQKILFEEQDLRKHGLGDEVSALFNWNIKDKINCERYVYGFH	487		
Db	288	-----RDLCSLAAGIWKQKTLFSPDDLRRKHLGDAIISTFLKMGILQEH-PIPLSYGFH	342		
Qy	488	LSFOEFPAAMYIILDEGEGGAGPDQ-----DVTLLLEYAFSPERSFLATLSRFLFGLNNEE	543		
Db	343	LCQEFPAANSYVL-EDEKGRGKHSNCIIIDEKTLKLEAYGI-HGLFGASTTFFLLGLLSDE	400		
Qy	544	TRSHLEKSLCWKVSPIHKMDLLQWIOSKAQSDGSLQOGSLEFPSCFYIETQEEFFIOQAL	603		

513 --DVTRLLTEYAFSSERELATSRFLGCLLNEETRSLEKSLKWKVSPHIMKMDLLOWIQS 570
522 FIENQRSIMEVTRTDDTRLLGKRFELGLMKDKILKTLVLFEYVPVTPVQKQLQHWVSL 581
571 KQSDGSTLQOQSDFEFCLEIEBEEFIOALSHFQVIVVSNIASKMEHNVSSPCLKRC 630
582 IAQVNGTSPMDTDAFYCLPESODEEFGVGGALKRFOEVWLL-INQKMDLVSSYCLKHC 640
631 RSAQVHL-----YCATYSADGE----- 648
641 QNLKAIKRDVIRDLSDVNTLELCPVVVTOETOCKPLLMWGNFCVLSGLSLNLKELDLG 700
649 DRARCSAGAHLLVQLRPE-----RTVLDDAYSEHLAAALCTNPNLIELSLYRNAL 699
701 DSILSQBANKILCLERNSCRIQLTFKSAEVSGLKHLWKLFSNQNLKYLNLGNTPM 760
700 GSRGVKLLCOGLRHPNCKLQNLKRCRISSACEDLSAALTANKNLTRMDLSGNGVQFP 759
761 KDDMKLACEALKHPKCSVETLRLDSCETLTIGYEMISTLLISTTLKCLSLAKNRVGVK 820
760 GMLLCEGLRHPQCRLOMIOLRKCQLESGACQBSMASVLGTNPVHPLVELDTGNALEDGLR 819
821 SMISLGNALSSMCLLQKLLDNCGLTPASCHLLVLSALFSNQNLTHLCLSNLSLGEVQ 880
820 LLCQGLRHPVRLRLTLMLKICRTAAACDELASTLSVNSQSLRELDLSLNLGDLGVLLLC 879
881 QLCQFLRNPICALQRLILNHCNIVDDAYGFLAWRLANNNTKLTLSLTMVPGVGAMKLLC 940
880 EGLRHPCKLOTLRIGICRLGSAACEGLSVVLOANHNRLDELDSFNDLGMWGLWLLAEG 939
941 EALKEPTCYLOLELVDQCLTQCCEDLACMIITTKHLKSLDLGNALGDKGVITLCEGL 1000
940 QHPACRLCKWLDSGLTAKACENLYFTLGINQTLDTLYLTNNALGDTGVRLCKLSHP 999
1001 KQSSSLRLRLGLGACKLTSNCCALSLAISCNPHLSNLVKNDFSTSGMLKLSAFQCP 1060
1000 GCKRLVWLFGLNDLKNMTHSLAALRVTKPYLDI 1033
1061 VSNLGIILGWKQEVYARVRQRLEVEFVKPHVVI 1094

RESULT 3
A1858
ribonuclease-angiogenin inhibitor - human
N;Alternate names: ribonuclease inhibitor, placental
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence, revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: A31858; S02012; S23933; S48636; T47188
R;Lee, F.S.; Fox, E.A.; Zhou, H.M.; Strydom, D.J.; Vallee, B.L.
Biochemistry 27, 8545-8553, 1988
A;Title: Primary structure of human placental ribonuclease inhibitor.
A;Reference number: A31858; MUID:89118269; PMID:3219362
A;Accession: A31858
A;Molecule type: mRNA
A;Residues: 1-461 <LEE>
A;Cross-references: UNIPROT:P13489; GB:M22414; NID:G186260; PIDN:AAA59130.1; PID:G30704.
R;Schneider, E.; Schneider-Scherzer, E.; Thurnher, M.; Auer, B.; Schweizer, M.
EMBO J. 7, 4151-4156, 1988
A;Title: The primary structure of human ribonuclease/angiogenin inhibitor (RAI) disclos
A;Reference number: S02012; MUID:89210799; PMID:3243277
A;Accession: S02012
A;Molecule type: mRNA
A;Residues: 1-422, 'SE', 425-461 <SCH>
A;Cross-references: EMBL:X13973; NID:G35843; PIDN:CAA32151.1; PID:G35844
A;Note: part of this sequence, including the carboxyl end of the mature protein, was co
R;Crevel-Thieffry, I.; Cotterill, S.; Schuller, E.
Biochim. Biophys. Acta 1122, 107-112, 1992
A;Title: Characterisation of a tryptic peptide from human placental ribonuclease inhibi
A;Reference number: S23933; MUID:92338217; PMID:1633192
A;Accession: S23933
A;Molecule type: protein
A;Residues: 174-195 <CRE>
R;Nadano, D.; Yasuda, T.; Takeshita, H.; Uchida, K.; Kishi, K.

401 GEREMENIFHCRLSQ--GRNLQWVPSLQ-----LLLOPHSLLESLSLCHLYETRNKTLFTQVM 454
604 SHFQVIVVSNIAKMEHNVSSFCLEKCRSAQVHLHYGATYSADGEDRARCAGAHLLVQ 663
455 AHEEMGMC-VETDMELLVCTFCIKPSRHVKQLQI-----BGRQHRSTWSTWVVL 505
664 LRPBTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRGVLLCOGLRHPNCKLQNLRL 723
506 FR--WVPVTVDAYWQILFVSLKVRNLKELDLSGNSLSHSAVSKLCKTLRPRCLLETLR 563
724 KRCRISSACEDLSAALTANKNLTRMDLSGNGVGFPGMMLLCEGLRHPQCRLOMLQKRC 783
564 AGCGLTADCKDLAFLGRANQTLTDLSPNVLTDAKXHLQORLQROPCKLQRLQVSC 623
784 QLESGACQEMASVLGTNPVHPLVELDTGNALEDGLRLCOGLRHPVRLRLTLMLKICRLT 843
624 GLTSDCCDLASVLSASPSLKELDQNNLDDGVRLLCGLRHPACKLIRLGL----- 677
844 AAACDELASTLSVNSQSLRELDLSLNL-----GDLGVLLLCEGL-----RHPTCKLOTUR 893
678 ----DQTLSDQMQLRALQEKPOLLIISRKKPSVMTPTGLDTGEMSNSTSLRQR 733
894 LGICRLGSAACEGLSVVLOANHNRLDELDS 923
734 LGSERAASHV-----AQNKLKLDVS 754

RESULT 2
A59000
mater protein [imported] - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
R;Tong, Z.B.; Nelson, L.M.
Endocrinology 140, 3720-3726, 1999
A;Title: A mouse gene encoding an oocyte antigen associated with autoimmune premature ov
A;Reference number: A59000; MUID:99360614; PMID:10433232
A;Accession: A59000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1111 <KUR>
A;Cross-references: UNIPROT:Q9RLM5; GB:AF074018; NID:G5802697; PIDN:AA051762.1; PID:G580
C;Genetics:
A;Gene: Mater

Query Match 21.2%; Score 1160.5; DB 2; Length 1111;
Best_Local Similarity 31.4%; Pred. No. 1.9e-81;
Matches 293; Conservative 165; Mismatches 407; Indels 69; Gaps 13;
162 HQASP-IX-IETLEPDEERPEPRTVWQGAAGICKSMIAHKVMDLWADGKLFQGRFDY 219
168 HYDSPMKLLSDAFKP-YQKTFQPHITLHGRFVGKKSALARSIVLQWAGKLFQ-KMSF 225
220 LFVINCENMOSATECSMQDLIFSCWPEPSAPLOELIRVPERLLFIIDGDELKPSFHPD 279
226 VIFPSVREIKWT-EKSSLAQLIAKECDSDMLVTKIMSQPERLLFVIDGLDMDSDVLQHD 284
280 QGPWCLCWEKRPTELLNSLIRKILPELSLITTRPTALEKHLRLLEHPRHVEILGFS 339
285 DMTLSRDKRQPIYILMYSLLRALLPQSFLLITTRNTGLEKLSKWVSPYLVEGLS 344
340 EAERKEYFYKFNHAEQAGQVFNVRNEPLFTWCFVPLVCVWVCTCLOQLEGGGLLRQ 399
345 AGRRQLVLENISNESDRIQVHSLIENHQLFDQCAPSVCSLVCEALQLOKLGKRCRTL 404
400 TGRITAVY---MLYLLSIMPQKCAPLQPPNQRGICSLAADGLWKNOKILPEEODLRK 456
405 PCOTLTGLYATLVFPHQLTKRPSQALSQEBQITLVGLCMWAGVMTWSVFDYDLDKN 464
457 HGLDGDGVAFNLMMI-FQKINCERYYSFIHLSFQEFPAAMYVILDEGGGAGPDQ--- 512
465 YLSKESEIALFHMILLQVGNHNSQCYVFSHLSLDQFFAALYVYL---EGLEEWNHQFC 521

Arch. Biochem. Biophys. 312, 421-428, 1994
A>Title: Purification and characterization of human brain ribonuclease inhibitor.
A;Reference number: S48636; MUID:943111593; PMID:8037455

A;Accession: S48636

A;Status: preliminary

A;Molecule type: protein

A;Residues: 2-14 <NAB>

R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.

submitted to the Protein Sequence Database, March 2000.

A;Reference number: 224374

A;Accession: T47188

A;Status: preliminary

A;Molecule type: mRNA

A;Cross-references: EMBL:AL161967

A;Experimental source: adult testis; clone DKFp434K249

C;Genetics:

A;Gene: GDB:RNH

A;Cross-references: GDB:125274; OMIM:173320

A;Map position: 11p15.5-11p15.5

A;Note: DKFp434K249.1

C;Superfamily: ribonuclease inhibitor; leucine-rich alpha-2-glycoprotein repeat homology

C;Keywords: blocked amino end; duplication

F;34-433/Region: leucine-rich 57-residue repeats

F;57-81/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F;114-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F;174-195/Region: inhibitory

F;228-252/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F;285-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F;399-423/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

Query Match 13.2%; Score 724; DB 2; Length 461;

Best Local Similarity 42.5%; Pred. No. 4.1e-48;

Matches 150; Conservative 64; Mismatches 139; Indels 0; Gaps 0;

Qy 671 LLDAYSEHLAAALCTNPNIELSILYRNALSGRGVKKLCOGLRHPNCKLQNLRLKRCRISS 730

Db 40 LTEARCKDISSALRVNPAELNLSNELGVDGVHCVLQGLQTPCKIQKLSLQNCCLTG 99

Qy 731 SACEDLAAALIANKNLTRMDLSNGVGFPGMMLCEGLRHPQCRLOMIQRLKCKOLESGAC 790

Db 100 AGCGVLSPDLTFTLQELHLSNDLGDAGLQLCEGLDPOCKLEKIQLEYCSLSAASC 159

Qy 791 QEMASVLGTNPVHVELDLTGNALEDLGLRLCCOGLRHPVCRRLTLWLKICRLTAACDEL 850

Db 160 EPLASVLRAPKDFKELTVSNNDINEAGVRLVLCQGLKDSQPCLEALKLESQVTSNDCRDL 219

Qy 851 ASTLSVNQSLRELDLSNELDGLVLLCEGLRHPNCKLQNLRLKRCRISS 910

Db 220 CGIVASKASRELALGSKLGDVGMALCPGLLHPSSRLRLTLWECGITAAGCGDLCRV 279

Qy 911 LOAHNHLRELDLSFNDLGDGLWLLAEGLQHPACRLQKLDSCGLTAKACENLYFTLGI 970

Db 280 LRKESKELSLAGNELGDEGARLLCETLLEPGQLESLSLVKSCSFTAACCSHPSVLAQ 339

Qy 971 NOTLTDLYLTNNALGDTGVRLCKRLSHPGCKLRVLMFGMDLNKMTSHSLAA 1023

Db 340 NRFLLEQLISNNRLEDAGVRELCCGLGQPGSVLRVLMADCDVSDSSCSLAA 392

RESULT 4

S20597

ribonuclease inhibitor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S20597

F;Kawanomoto, M.; Motojima, K.; Sasaki, M.; Hattori, H.; Goto, S.

Biochim. Biophys. Acta 1129, 335-338, 1992

A>Title: cDNA cloning and sequence of rat ribonuclease inhibitor, and tissue distribution

A;Reference number: S20597; MUID:92162755; PMID:1536887

A;Accession: S20597

A;Molecule type: mRNA

A;Residues: 1-456 <KAW>

A;Cross-references: UNIPROT:P99315; EMBL:X62528; NID:957670; PIDN:CAA4388.1; PID:95767
C;Superfamily: ribonuclease inhibitor; leucine-rich alpha-2-glycoprotein repeat homology
F;280-304/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 13.1%; Score 717; DB 2; Length 456;

Best Local Similarity 41.5%; Pred. No. 1.4e-47;

Matches 147; Conservative 66; Mismatches 141; Indels 0; Gaps 0;

Qy 671 LLDAYSEHLAAALCTNPNIELSILYRNALSGRGVKKLCOGLRHPNCKLQNLRLKRCRISS 730

Db 35 LTVRCKDIRSAIQANPALTELSLRTNELGDAGVGLVQLQNPCTCKIQKLSLQNCSLITE 94

Qy 731 SACEDLAAALIANKNLTRMDLSNGVGFPGMMLCEGLRHPQCRLOMIQRLKCKOLESGAC 790

Db 95 AGCGVLSPDLVRLSLTLRELHNDNPLGDEGLKLLCEGLRDPQCRLEKIQLEYCNLTATSC 154

Qy 791 QEMASVLGTNPVHVELDLTGNALEDLGLRLCCOGLRHPVCRRLTLWLKICRLTAACDEL 850

Db 155 EPLASVLRVRPDKFELVLSNNDFHEAGIHTLCQGLKDSACQLESKLUENCGITTSANCKDL 214

Qy 851 ASTLSVNQSLRELDLSNELDGLVLLCEGLRHPNCKLQNLRLKRCRISS 910

Db 215 CDVVASKASLOELDLGSKNLGNTGIAALCSGLLLPSCRLRTLWLDGCVTAEGCKDLCRV 274

Qy 911 LOAHNHLRELDLSFNDLGDGLWLLAEGLQHPACRLQKLDSCGLTAKACENLYFTLGI 970

Db 275 LRKQSLKELSLAGNELKDEGAQLLCESLLEPGQLESLSLVKTCSLTAASCPHFCSVLTK 334

Qy 971 NOTLTDLYLTNNALGDTGVRLCKRLSHPGCKLRVLMFGMDLNKMTSHSLAA 1024

Db 335 NSSLIFELQSSNPLGDSGVVELCKALGYPTVLRVLMWLDGCDVTDSCSSSLATV 388

RESULT 5

A31857

ribonuclease inhibitor, hepatic - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C;Accession: A31857; A35830

R;Hofsteenge, J.; Kieffer, B.; Matthies, R.; Hemmings, B.A.; Stone, S.R.

Biochemistry 27, 8537-8544, 1988

A>Title: Amino acid sequence of the ribonuclease inhibitor from porcine liver reveals t

A;Reference number: A31857; MUID:89118268; PMID:3219361

A;Accession: A31857

A;Molecule type: protein

A;Residues: 1-456 <HOF>

A;Cross-references: UNIPROT:P10775

R;Vicentini, A.M.; Kieffer, B.; Matthies, R.; Meyhack, B.; Hemmings, B.A.; Stone, S.R.,

Biochemistry 29, 8827-8834, 1990

A>Title: Protein chemical and kinetic characterization of recombinant porcine ribonucle

A;Reference number: A35830; MUID:91104783; PMID:2271559

A;Accession: A35830

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 82-456 <VIC>

A;Cross-references: GB:M58700; NID:6164638; PIDN:AAA63448.1; PID:6164639; GB:J02925

C;Superfamily: ribonuclease inhibitor; leucine-rich alpha-2-glycoprotein repeat homology

C;Keywords: liver

F;280-304/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 13.0%; Score 709; DB 2; Length 456;

Best Local Similarity 42.7%; Pred. No. 5.8e-47;

Matches 151; Conservative 60; Mismatches 143; Indels 0; Gaps 0;

Qy 671 LLDAYSEHLAAALCTNPNIELSILYRNALSGRGVKKLCOGLRHPNCKLQNLRLKRCRISS 730

Db 35 LTBHECKDIGSALRANPSLTCLRLTNELGDAGVHLVQLQSPCTCKIQKLSLQNCSLITE 94

Qy 731 SACEDLAAALIANKNLTRMDLSNGVGFPGMMLCEGLRHPQCRLOMIQRLKCKOLESGAC 790

Db 95 AGCGVLSPDLVRLSLTLRELHLSNDNPLGDEGLKLLCEGLRDPQCRLEKIQLEYCNLTATSC 154

Qy 791 QEMASVLGTNPVHVELDLTGNALEDLGLRLCCOGLRHPVCRRLTLWLKICRLTAACDEL 850

Db 155 EPLASVLRATRALKELTVSNNDIGEAGARVLGQGLADSACQLETLRLNCGLTTPANCKDL 214
Qy 851 ASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPTCKLQTLRLGCRIGLSAACGLSVV 910
Db 215 CGIVASQASLRELDLSNGLDGAGIAELCPGLSPASRLKTLWLWECDDTAGCRDLCEV 274
Qy 911 LOAHNHLRELDLDFNDLGDWGLWLLAEGLOHPACRIQLKWLDSCGITAKACENLYFTLGI 970
Db 275 LQAKETLKSLAGNKLGDGALLCESLLQPCQLESLLWVKSLSLTAACQHVLSMLTQ 334
Qy 971 NOTLTDLYLNALGDTGVRLCKRLSHPCCKLRLVWLFQMDLNKMTKTHRLAAL 1024
Db 335 NKHLELQLSNKLSDSGIQELQALSQPGTTLRLVLCLGDCVNTNSGCSLASL 388

RESULT 6
S27880
Nasopressin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C:Accession: S27880
R:Herrera, V.L.; Ruiz-Opazo, N.
A:Description: Characterization of a cDNA encoding an AII and AVP receptor isoform.
A:Reference number: S27880
A:Accession: S27880
A:Molecule type: mRNA
A:Residues: 1-483 <R>
A:Cross-references: EMBL:M85183; NID:G202805; PIDN:AAA03623.1; PID:G202806
C:Genetics:
A:Gene: AVP

Query Match 9.0%; Score 494.5; DB 2; Length 483;
Best Local Similarity 28.8%; Pred. No. 2.9e-30;
Matches 147; Conservative 74; Mismatches 205; Indels 85; Gaps 10;

RESULT 7
A48843
MHC class II transactivator - human
N:Alternate names: CIITA
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: A48843
R:Steinle, V.; Otten, L.A.; Zufferey, M.; Mach, B.
Cell 75, 135-146, 1993
A:Title: Complement cloning of an MHC class II transactivator mutated in hereditary
A:Reference number: A48843; MUID:94006536; PMID:8402893
A:Accession: A48843
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1130 <STE>
A:Cross-references: UNIPROT:P33076; GB:X74301; NID:G414112; PIDN:CAA52354.1; PID:G41411

Query Match 6.9%; Score 377.5; DB 2; Length 1130;
Best Local Similarity 23.6%; Pred. No. 1.2e-20;
Matches 220; Conservative 122; Mismatches 355; Indels 235; Gaps 40;

Qy 92 EDLVDPQETY-----RDYVRKRLMEDNARILGECVNLSHRYTRLLLVKEHSNPMQV 145
Db 339 EQFYRLQDTYGAEPAGDPDGLVEVLVQ---ARL-----ERSSSKSLERELATPDWA 388
Qy 146 QOQLDTCGRHARTVGHQASPIKTIETLPEDEERPEPPTVVMQGAAGIGKSLAHKVMY 205
Db 389 ERQLAQGGAEV-----LLAAKEHRRPRETRVIAVLGKAGQGSYWAGAVSR 435
Qy 206 DWADGKLFQGRFDYLYINCREMOSATECSMODLIFSCWPEPSAPLOE-----LIRVPER 261
Db 436 AMACRLPQ--YDFVFSVPCHLNRPDAYGLQDLFLSLGPQLVAADEVFSLHKRPDR 493
Qy 262 LIFIDPDELKPS---HDPQGPWLCWEKKRPEL--LLNSLRKLLPELSLITTR 316
Db 494 VLLIILDAFEEAQAQGFLLHSTCGP-----APAPCSLRLGLAGLFQKLLRGCTLLLTAR 548
Qy 317 P-----TALEKILRLLEHPRHVEIILGFSEAEKKEYFYKFHNA-----EQAGQVNVVRNE 368
Db 549 PRGLRVOSLSKADALF-----ELSGFSMEQAQVVMRYFSSGTMTEHQDRALTLLDRP 602
Qy 369 PLFTMCVPLVWVCTCLQOQLEGGLLRQTSRTTAVMYLLSLMQPKGAPRLQPP 428
Db 603 LLLSHSPTLCRAVCQLSEALLELGEDAKLPS--TLTGLYVGLL-----GRAALDSP 653
Qy 429 ENQRG--LCSLAAD--GLMNOKILFEEQ-----DLR-----KHGLDGEDVSAFLNMNIFQKQIN 478
Db 654 PGALAEALAKLAWELGRHHQSTLQEDQFPSPADVRTWMAKGLVQHPPRA----- 701
Qy 479 CERYYSFIHLSFQEPFAAMYIILDEGEGAGDPDQDVTLLTTEYAFSEF-----SFLALTSHF 535
Db 702 AESELAFFSFLQCPLGALWAL-----SGEIKDELPOVLALTPRKKRPYDNWLEGVPRF 757
Qy 536 LFLGLNNEETRSHLEKSLCWKSPHICKDILLQIQS---KAQSDGSTLQOQSLFEFFSCLYE 592
Db 758 LAGLIIFQPPARCIGALL--GPSAAASVDRKQKVLARYLKLQPGTILRAQLLELLHCAHE 815
Qy 593 IQEEEFITQALSHFQIVVSNIAKSMHVMVSSFLKRCRSAQVLIHLYGATYSADGEDRAR 652
Db 816 AEAAGIQH-----VVQELPGRLL-----SFLGTRLTTPDA--HVLGKALEAAGQD--- 858
Qy 653 CSAGANTLIIVQLRPERTVLLDAYSEHLAAALCTN--PNLIELSL---YRNALGSRGVKLL 707
Db 859 -----FSLDLR-----STGICPSGLSVGLSCVTRFRAALSD--TVAL 895
Qy 708 COGLR--HPNCKL-----QNL--RLKRCRISSACEDISAALIANK 744
Db 896 WESLRQGETKLLQAAAEKEFTIEFPFAKSLKDVEDLGLVQVQTRTSSSEDTAGELPAVR 955
Qy 745 NLTRMDLSNGVGFPPGMMLLCEGLRHPQCRQLQMLQIRKCOLESGACQEMASVLTGTPHLY 804
Db 956 DLKKLEFALGVSPGQAF-----PKLV 977


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Db 221 QMKLHPDYRPTSI FEVLGLLEAKNNL-----GTQLCGEYPAIKTLDQOPNAHL 274
QY 375 FVPLVCMVCTCQQQLQEGGLLRQTSRTTAVYMLYLLSLMQ-----PKPGAPR 424
Db 275 YLPINFILVFCULSN-EGSDI-----KWTQVLIFSMTRFVELSHLKEVPLDKVGAEM 328
QY 425 LQPPPNQRGLCSLAADGLMNQKILFEEQDLRKHLGDG-----DVSAFLANNIFQ 474
Db 329 VK-----LARLAYKGLQKLVFEKTFDDVKLADVMVTFPHFYVDKSGIRMKILE 381
QY 475 KOINCERYYSFIHLSFOEPPAAMYIILDEGEGAGPDQDVTRLLTTYAESSEFLAL---- 531
Db 382 GN---KRSY-FTHLIWQEFYAAYLML-----FVSREFEOLKPI 417
QY 532 -----TSRELFGLLNEETRSHLEKSLCWKYSVP-----HIKMDLLQWQSKAQSDG 576
Db 418 FKDAQKRVVGFPGICNPPAYQOLK-----LVFPATMIKDYEEKELM--VPMMESLW 470
QY 577 STLQOGLSEFFSCLYEIQEEFIQOALSHFOV---IVVSNIAKMHVSSFCLEKCRSA 633
Db 471 SARGEDLIRRFGLWHEYNDESSKKFEDYLPVGLKMDAPKHLSEVKDLV--YALKSFTRP 528
QY 634 QVLHL--YGATYSADGEDRARCAGATLAV-----QLRP 666
Db 529 HKLRDSYETTTETVETLRLRGVHGTTTTITRFVNNIEMKDSLMELLLLHLDAEELRF 588
QY 667 ERTVLLDAYSEHLAAALCTPNPILIELSLYRNAL--GSRGVKLL--COGLRHPNCKLQNLRL 723
Db 589 IRVTNLSPYMERLSNAINQSRNKIQLVLIKHKLHDDYDVYKLAGCLG-----NISLLYM 642
QY 724 KCRISISSACEDLSAAL 740
Db 643 WGTDISSDQCSVLKQAI 659

RESULT 10
A55478
neutrol apoptosis inhibitory protein - human
N:Alternate names: NAIP
C:Species: Homo sapiens (man)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C:Accession: A55478
R:Roy, N.; Mahadevan, M.S.; McLean, M.; Shuttler, G.; Varaghi, Z.; Parahani, R.; Baird, S.
d., T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; Mackenzie, A.
Cell 80, 167-178, 1995
A:Title: The gene for neuronal apoptosis inhibitory protein is partially deleted in indi
A:Reference number: A55478; MUID:95112344; PMID:7813013
A:Accession: A55478
A:Molecule type: mRNA
A:Residues: 1-1232 <ROY>
A:Cross-references: GB:U19251
C:Genetics:
A:Gene: GDB:SMA@; SMA
A:Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A:Map position: 5q12.2-5q13
C:Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-loop; transmembrane prot
F:94-110/Domain: transmembrane #status predicted <TM1>
F:470-477/Region: nucleotide-binding motif A (P-loop)
F:479-496/Domain: transmembrane #status predicted <TM2>
F:476/Binding site: ATP (lys) #status predicted
F:618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 3.4%; Score 183.5; DB 2; Length 1232;
Best Local Similarity 21.3%; Pred. No. 1.6e-05;
Matches 148; Conservative 94; Mismatches 248; Indels 205; Gaps 35;

QY 188 MCGAAGIGKSLAHKVMLDWADKGL-FQGRFDYLFYINCR-----EMN 229
Db 468 VEGEAGSGTVELLKIAFLWASCCPLLNRFLVFLVLSLRPRDEGLASITCDQLLEKE 527
QY 230 QSATECSMODLIFSCWPEPSAPLOELIRVPERELLIIIDGFDLKPSPHDPQPCWCLWEE 289

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Db 528 GSVTEMCMRNII-----QQL---KNQVFLFLDDYKEI---CSIQP----- 561
QY 290 KRPTELLNSLIRKLLPELSLLITTPTALEKHLRLEHPRHVILGFESEAEKKEYFK 349
Db 562 -----VIGKLIQKNHLSRTCLLIIVATNRARDIRRYLE--TILEIOAFP-----FYN 606
QY 350 -----YFNASQAGQVFNVRDNEPLFTMCVFPLVVCVVCT-CLQQQLGEGGLLRQT 400
Db 607 TVCILRKLSFNSMTRLRKFVYFGKNSLOKIQTPLFVAACAHWFQYPPD-----P 659
QY 401 SRTTAVYMLYLLSL-MOPKPGAPRLOPPNQRLGCSLAADGLMNQKILFEEQDLRKHL 459
Db 660 SFDDVAVPKSYMERLSLRNKATAILKATVSSCG--ELALKGFESCCFEFNDDDLAEGV 717
QY 460 DGEDVSAPLNNI FQKDINCERYYSFIHLSFOEFAAMYI--LDEGEGGAGPDQDV--- 514
Db 718 DEDEDLTWCLMSKFTAQ-RLRPFYRFUSPAFOEFLAGMRLIELLDSR---QEHQDLGLY 773
QY 515 -----TRLLTEYAF-----SERSFLALTSLRFLGLLNEETRSHL----- 548
Db 774 HLKQINSPMVTVSAXNNFLNVVSSLPSTKAGPKIVSHLLHLVDNKNESLENISENDDYLKH 833
QY 549 --EKSL-----CWKVSPIHKMDL-----LQMTOSKQAQ 573
Db 834 QPEISLQMLLRGLMQICFOAYFSVMVSEHLLVLALKTAQSNVTAACSPFVLQFLQ---- 889
QY 574 SDGSTLQOGLSEFFSCLYEIQEEFIQOALS-HFOVIVVSNIAKMHVSSFCLEKRCR 631
Db 890 --GRTLTTLGAL---NLQYFFDHPESLSLRSIHFS--IRGNKTSFRAHFSVLETCFDSQ 942
QY 632 SAQVHLHYGATYS-----ADGED-----RARCAGATLVLQRLPERTVL--- 671
Db 943 VPTIDODYASAPEPMNEWERNLAEKEDNVKSYMDMQRASPDLSLTYWKLSPKQYKIPCL 1002
QY 672 -----LDAYSEHLAAALCT---NPNLIELSLYRNALGSRGVKLLCOGLRHPNCKLQNLRL 722
Db 1003 EVDVNDIDVVGQDMLEILMTVFSASQRIELHNLH-----SRG---FIESIR-PALELSKAS 1054
QY 723 LKCRISISSACEDLSAA-----LIANKNLTRMDLSG 753
Db 1055 VTKCSISKL---ELSAAEQELLLTLPSSLESLEVSQ 1086

RESULT 11
B97746
hypothetical protein RC0370 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97746
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.;
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: B97746
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <KUR>
A:Cross-references: UNIPROT:Q921Q0; GB:AE006914; PIDN:AAL02908.1; PID:g15619435; GSPDB:
C:Genetics:
A:Gene: RC0370

Query Match 3.3%; Score 180; DB 2; Length 312;
Best Local Similarity 19.0%; Pred. No. 4e-06;
Matches 64; Conservative 74; Mismatches 117; Indels 82; Gaps 12;

QY 97 DPQETRYDYVRRKFRMLMDNRNARLGBCVNLSHRY-----TRLLVKEHENPMQ 144
Db 34 DTEAKIREWFDKYNQVEEKIDNIAKSLNEENKFAILLRNLTNKTSTSEIKNIVEKINRMQ 93
QY 145 VQOQLDLTGRTGHARTVGHQASPIKIEITLFPDEERPEPPTVYVMOGAGIGKSLAHKVM 204
Db 94 V-----DIGK-----VLLLSAGIGKTLTLMHYLS 117

```


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Qy 630 CRSAQVHLHYGATYSADGEDRARCAGAHLLVQLRPERTVLLDAYSEHLAAALCTNPNL 689
Db 249 CGNNFENWLEFYY-RDCYSLAATIKACHTKI-PKLTREKVDKARILIRSLDHPAL 306
Qy 690 IEISLYRNALSGRGVKKLCOGLRHPNCKLQNLRLKRECRSSACEDLSAALANKNLTRM 749
Db 307 EELDLSHNLIGDRGARAANKLLSH----- 330
Qy 750 DLSGNGVGFPGWMLLCEGLRHPQCRLQIOLKRCQESGACQEMASVLTGPNPHVLELDIT 809
Db 331 -----SRLRVNLANNQLOAPGAQSLAHALAHNTNLVFLNLR 367
Qy 810 GNALEDLGLRLCQGLRHPVCRILTLMKICRTATAACDELASTLSVNOSIRELDLSLNE 869
Db 368 LNCIEDEGGAIAHALETNKC-LSVLHLGKNLSEPTATILLSQMLTNTTTLVSLNLSCHN 426
Qy 870 LGDLGVLLCEGLRHPFCKQLTLRLGICRLGSAACEGLSVLQANHNLRELDLSFNDLGD 929
Db 427 IGQDG-----GKQLLEGIS-----DNKTILEFDLRLSDVSQ 457
Qy 930 WGLWLLAEGL 939
Db 458 ESEYLIGQVL 467

RESULT 15
T48193
hypothetical protein F7A7.240 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48193
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Daseville, R.; De
ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24487
A:Accession: T48193
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-618 <BEV>
A:Cross-references: UNIPROT:Q9M004; EMBL:AL161946
A:Experimental source: cultivar Columbia; BAC clone F7A7
C:Genetics:
A:Map position: 5
A:Introns: 213/3; 255/3; 259/3; 294/3; 350/1; 376/1; 419/2; 517/3; 601/3
A:Note: F7A7.240

Query Match 3.2%; Score 172.5; DB 2; Length 618;
Best Local Similarity 25.4%; Pred. No. 4.1e-05;
Matches 122; Conservative 61; Mismatches 160; Indels 137; Gaps 28;
Qy 629 RCRSAQVHLHYGATYSADGEDRARCAGAHLLVQLRPERTVLLDAYSEHLAAALCTNPN 688
Db 123 KCVNLVEIDLSNATERDAD--AAVVAEARS--LERKLGRCMKLTDMGICGIAVGCKLN 179
Qy 689 LIELSLYRNALSGRGVKKL---COGLR-----HPNCKLQNLRLKRC-- 726
Db 180 TVSLK-WCVGVGDLGVGLLAVKCKDIRTLDSYLPITGCKLHDILKQLHEELLEGGCFG 238
Qy 727 -----RISSACEDLSAALIANKNLTRMDLSCNGVGFPGWMLLC 765
Db 239 VDDDSLKSLRHDCSKLWKYKQLDASSCQNL-----HRGLTSL--LSGAGY----- 283
Qy 766 EGLRHPQCRLQIOLKRCQESGACQEMASVLTGPNPHVLELDITGNALEDLGLR---LLC 822
Db 284 -----LQRLDLSHC--SSVISLDPASSLKKVSALQSIRLDGCVTPDGLKAIGTLC 332
Qy 823 QGLRH-----PVCRLRTLWL--KICRLTAAACDELASTLSVNOSIRELDLSNELGDL 873
Db 333 NSLKEVSLSKCVSVTDEEAFWLIGQKRL-----LEELDITDNEIDD- 374
Qy 874 GVLLLCGLRHP-PTC-KIOTLRIGICRLGSAACEGLSVLQANHNLRELDLSFNDLGD--D 929
Db 375 -----EGLKSISSLSLSLKLIGLCL--NITDKGLSYIGMGCSNLRELDL--YRSVGITD 425

Qy 930 WGLWLLAEGLQHPACRLQKWLWDSC-GLTAKACENLVFTLGINQTLTDL---YLTNNALG 985
Db 426 VGISTIAQGCIIH-----LETINISYCQDITDKSLVSL-SKCSLLQTPESRGCPNITSQGLA 480
Qy 986 DTGVRLLECKRLSHPGCK-----LRVLWLFQMDLNKMTKTHSRLLAALRVTKPYL-DIGC 1035
Db 481 AIAVR--CKRLAKVDLKKCPISINDAGLLALAHFSQLKQINVSVDTAVTEVGLLSLANIGC 538

Search completed: February 8, 2005, 14:59:56
Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 14:29:33 ; Search time 185 Seconds
(without alignments)
2864.875 Million cell updates/sec

Title: US-10-781-294-24

Perfect score: 5472

Sequence: 1 MLRTAGRDGLCRSLSTYLEEL.....NTHSLAALRVTKPYLDIGC 1035

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

.Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5433	99.3	1061	1	NA12 HUMAN
2	2722	49.7	719	2	Q6UQE6
3	2396	43.8	1034	1	CS1L HUMAN
4	2359.5	43.1	1033	1	CS1L_MOUSE
5	2253.5	41.2	977	2	Q6TG35
6	1799	32.9	1093	1	NA14 HUMAN
7	1519.5	27.8	991	2	Q7RTR0
8	1505.5	27.5	986	2	Q6W27
9	1493.5	27.3	506	2	Q6U61
10	1475.5	27.0	506	2	Q6U59
11	1475.5	27.0	506	2	Q6U60
12	1474	26.9	500	2	Q6U56
13	1471	26.9	500	2	Q6U53
14	1470.5	26.9	506	2	Q6U57
15	1468.5	26.8	506	2	Q6U58
16	1461	26.7	500	2	Q6U51
17	1458	26.6	500	2	Q6U50
18	1457.5	26.6	994	1	NA14 HUMAN
19	1450.5	26.5	994	2	Q6W87
20	1449.5	26.5	499	2	Q6U55
21	1442	26.4	500	2	Q6U54
22	1438	26.3	500	2	Q6U52
23	1402	25.6	475	2	Q6U48
24	1401	25.6	1043	1	NA13 HUMAN
25	1396.5	25.5	993	2	Q6B966
26	1390.5	25.4	986	2	Q6X14
27	1387	25.3	1098	2	Q64719
28	1377	25.2	1375	2	Q6UB5
29	1375	25.1	1473	1	NA11 HUMAN
30	1320	24.1	1200	1	NA15 HUMAN
31	1314.5	24.0	287	2	Q9BY26

32	1309	23.9	1062	1	NAL2 HUMAN
33	1304	23.8	982	2	Q6X27
34	1299.5	23.7	437	2	Q6U49
35	1270.5	23.2	413	2	Q6JEK7
36	1268	23.2	978	2	Q6X19
37	1259	23.0	982	2	Q6U40
38	1251.5	22.9	413	2	Q6JEK9
39	1249.5	22.8	1048	2	Q7RTR4
40	1222	22.3	1009	2	Q7RTR1
41	1216.5	22.2	1029	2	Q6W28
42	1183	21.6	949	2	Q6X03
43	1168.5	21.4	1111	2	Q7PU9
44	1166.5	21.3	1095	2	Q6VSG3
45	1165.5	21.3	1111	2	Q6XZF2

ALIGNMENTS

RESULT 1
ID_NA12 HUMAN STANDARD; PRT; 1061 AA.
AC P59046; Q8NEU4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE NACHT-, LRR- and PYD-containing protein 12 (PYRIN-containing APAF1-like protein 7) (Monarch-1).
GN Name=NALP12; Synonyms=PYPAF7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22162427; PubMed=12019269; DOI=10.1074/jbc.M203915200;
RA Wang L., Manji G.A., Grenier J.M., Al-Garawi A., Merriam S.,
RA Lora J.M., Geddes B.J., Briskin M., Distefano P.S., Bertin J.;
RT "PYPAF7, a novel PYRIN-containing Apaf1-like protein that regulates activation of NF-kappa B and caspase-1-dependent cytokine processing.";
RT J. Biol. Chem. 277:29874-29880(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22451042; PubMed=12563287; DOI=10.1038/nrml019;
RA Tschopp J., Martinon F., Burns K.;
RT "NALP3: a novel protein family involved in inflammation.";
RN [3]
RP Nat. Rev. Mol. Cell Biol. 4:95-104(2003).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
TISSUE=Lymphoma;
RA Williams K.L., Linhoff M.W., Harton J.A., Ting J.P.Y.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Leukocyte;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng H., White J., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May mediate activation of CASP1 via ASC and promote
CC activation of NF-kappa-B via IKK.
CC -!- SUBUNIT: Binds to ASC with its DAPIN domain.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=1;
CC IsoId=P59046-1; Sequence=Displayed;
CC Name=2; Synonyms=11;
CC IsoId=P59046-2; Sequence=VSP_005524;
CC Name=3; Synonyms=111;
CC IsoId=P59046-3; Sequence=VSP_005523;
CC Name=4; Synonyms=IV;
CC IsoId=P59046-4; Sequence=VSP_009879;
CC -!- TISSUE SPECIFICITY: Detected only in peripheral blood leukocytes,
CC predominantly in eosinophils and granulocytes, and at lower levels
CC in monocytes.
CC -!- SIMILARITY: Contains 1 DAPIN domain.
CC -!- SIMILARITY: Contains 8 leucine-rich (LRR) repeats.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY095146; AAM18227.1; -;
DR EMBL; AY154467; AAO18163.1; -;
DR EMBL; AY116204; AAM75142.1; -;
DR EMBL; AY116205; AAM75143.1; -;
DR EMBL; AY116206; AAM75144.1; -;
DR EMBL; AY116207; AAM75145.1; -;
DR EMBL; BC028069; AAM78069.1; -;
DR HSSP; PL3489; 1A4Y.
DR Genew; HGNC:22938; NALP12.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0008656; F:caspase activator activity; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006919; P:caspase activation; NAS.
DR GO; GO:0050729; P:positive regulation of inflammatory response; NAS.
DR GO; GO:0050718; P:positive regulation of interleukin-1 beta s...; NAS.
DR GO; GO:0045381; P:regulation of interleukin-18 biosynthesis; NAS.
DR GO; GO:0008588; P:release of cytoplasmic sequestered NF-kappaB; IDA.
DR GO; GO:0007165; P:signal transduction; NAS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007091; LRR_RNinh.
DR InterPro; IPR007111; NACHT_NTPase.
DR InterPro; IPR004020; PAAD_DAPIN.
DR Pfam; PF00560; LRR; 7.
DR Pfam; PF05729; NACHT; 1.
DR Pfam; PF02758; PAAD_DAPIN; 1.
DR PRINTS; PR00019; LEUCINCHPT.
DR PROSITE; PS00824; DAPIN; 1.
DR PROSITE; PS00837; NACHT; 1.
KW Alternative splicing; ATP-binding; Leucine-rich repeat; Repeat.
FT DOMAIN 1 95
FT DAPIN.
FT DOMAIN 211 528
FT REPEAT 712 735
FT REPEAT 741 764
FT REPEAT 769 791
FT REPEAT 798 821
FT REPEAT 826 849
FT REPEAT 883 906
FT REPEAT 940 968
FT REPEAT 997 1020
FT NP_BIND 217 224
FT ATP (Potential).

FT	VARSPLIC	862	973	Missing (in isoform 3).
FT	VARSPLIC	976	1031	/FTId=VSP_005523.
FT	VARSPLIC	862	1031	Missing (in isoform 2).
FT	VARSPLIC	862	1031	/FTId=VSP_005524.
FT	VARSPLIC	862	1031	Missing (in isoform 4).
FT	CONFLICT	691	691	/FTId=VSP_009879.
FT	SEQUENCE	1061	AA; 120172	MM; 8C10APE4907C131B CRC64;
Query Match		99.3%	Score 5433;	DB 1; Length 1061;
Best Local Similarity		97.4%	Pred. No. 0;	
Matches 1034;	Conservative	0;	Mismatches	0; Indels 28; Gaps 2;
QY	1	MLRTAGRDGLCRSLTYLLEAEVAVLKKFKLYLGTATLGEKIPWGSMEKAGPLEMAQLL	60	
DB	1	MLRTAGRDGLCRSLTYLLEAEVAVLKKFKLYLGTATLGEKIPWGSMEKAGPLEMAQLL	60	
QY	61	ITHFGPEEAWRLALSTPERINRKLWEGQREDLVR-----	96	
DB	61	ITHFGPEEAWRLALSTPERINRKLWEGQREDLVR-----	120	
QY	97	---DPQETRYDYVREKFKLMEDRNARLGEVNLSHRYTRLLVKEHSPNMQVQQLDGTG	153	
DB	121	PRKDPQETRYDYVREKFKLMEDRNARLGEVNLSHRYTRLLVKEHSPNMQVQQLDGTG	180	
QY	154	RGHARTVGHQASPIKIETLFPDEERPEPRTVVMQGAAGIGKMLAHKVMLDWADGKLF	213	
DB	181	RGHARTVGHQASPIKIETLFPDEERPEPRTVVMQGAAGIGKMLAHKVMLDWADGKLF	240	
QY	214	QGRFDYLVINCENQATSCMODLIFSCWPEPSAPLOELIRVPERLLFTIDGFDLKL	273	
DB	241	QGRFDYLVINCENQATSCMODLIFSCWPEPSAPLOELIRVPERLLFTIDGFDLKL	300	
QY	274	PSFHDQGWCLCWEKRPTELLNSLRKLLPELSLLITTRPTALEKHLRLBPHRV	333	
DB	301	PSFHDQGWCLCWEKRPTELLNSLRKLLPELSLLITTRPTALEKHLRLBPHRV	360	
QY	334	EILGFSEAEKRYFYKYFHNAEQAGOVFNVDNPELFTMCVFPLVWVCTCLOOQLEG	393	
DB	361	EILGFSEAEKRYFYKYFHNAEQAGOVFNVDNPELFTMCVFPLVWVCTCLOOQLEG	420	
QY	394	GGILROTSRTTAVVMYLLSLMOPKAPRLOPPNORGLCSLAADGLWNOKILFEED	453	
DB	421	GGILROTSRTTAVVMYLLSLMOPKAPRLOPPNORGLCSLAADGLWNOKILFEED	480	
QY	454	LRKHGLDGEDVSAFLNMNIFQKDCINERYYSFIHLSFQEFFAAMYIILDEGEGGAPDQ	513	
DB	481	LRKHGLDGEDVSAFLNMNIFQKDCINERYYSFIHLSFQEFFAAMYIILDEGEGGAPDQ	540	
QY	514	VTLLTEYAFSERSFLALTSRFLFGLNEETSHLEKSLCWKVSPIHMKDILQWIOSKAQ	573	
DB	541	VTLLTEYAFSERSFLALTSRFLFGLNEETSHLEKSLCWKVSPIHMKDILQWIOSKAQ	600	
QY	574	SDGSTLQOQSLEFFSCLYEIQEEFTQQALSHFQVIVVSNIAASKMEHVVSSFLCKRCRA	633	
DB	601	SDGSTLQOQSLEFFSCLYEIQEEFTQQALSHFQVIVVSNIAASKMEHVVSSFLCKRCRA	660	
QY	634	QVLHLYGATYSADGEDRARCAGAHILLVOLRPERTVLDAYSEHLAAALCTNPNIELS	693	
DB	661	QVLHLYGATYSADGEDRARCAGAHILLVOLRPERTVLDAYSEHLAAALCTNPNIELS	719	
QY	694	LYRNALSGRGVKKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG	753	
DB	720	LYRNALSGRGVKKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG	779	
QY	754	NGVGFPGMMLLCEGLRHPQCRLOMIQLRKQLESGACQEMASVLTGNPHLVELDLTGNAL	813	
DB	780	NGVGFPGMMLLCEGLRHPQCRLOMIQLRKQLESGACQEMASVLTGNPHLVELDLTGNAL	839	
QY	814	EDLGLRLLCOGLRHPVCLRTLMKICRLTAACADELASTLSVNQSLRELDLSINELGDL	873	
DB	840	EDLGLRLLCOGLRHPVCLRTLMKICRLTAACADELASTLSVNQSLRELDLSINELGDL	899	


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Qy 874 GVLLCEGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRRLDLSFNDLGDWGLW 933
Db 900 GVLLCEGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRRLDLSFNDLGDWGLW 959
Qy 934 LLAEGLOHPACRLQKLDSCGLTAKACENLYFTLGINQTLTDLTLTNALGDTGVRLLC 993
Db 960 LLAEGLOHPACRLQKLDSCGLTAKACENLYFTLGINQTLTDLTLTNALGDTGVRLLC 1019
Qy 994 KRLSHPGCKRLVLFGLMDLNKMTSHRLAALRVTKPYLDIGC 1035
Db 1020 KRLSHPGCKRLVLFGLMDLNKMTSHRLAALRVTKPYLDIGC 1061

RESULT 2
Q6UQE6 PRELIMINARY; PRT; 719 AA.
AC Q6UQE6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE NALP12 (Fragment)
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY364010; AAQ3460.1; -
DR InterPro; IPR003590; LRR_Rninh_sub.
DR InterPro; IPR007111; NACHT_NTPase.
DR InterPro; IPR004020; PAAD_DAPIN.
DR Pfam; PF05729; NACHT_1.
DR Pfam; PF02756; PAAD_DAPIN; 1.
DR SMART; SM00368; LRR_R1; 1.
DR PROSITE; PS00824; DAPIN; 1.
DR PROSITE; PS00837; NACHT; 1.
FT NON TER 719
SQ SEQUENCE 719 AA; 82623 MW; CA2E777CE7CC4A1F CRC64;

Query Match 49.7%; Score 2722; DB 2; Length 719;
Best Local Similarity 71.1%; Pred. No. 3.8e-185;
Matches 517; Conservative 81; Mismatches 115; Indels 14; Gaps 3;

Qy 1 MLRTAGDGLCRSLTYLEELAEVLEKFKLYLGTATLGEKIPGWSKAGPLEMAQLL 60
Db 1 MLPSTARDGLVRLTYLEELAEVLEKFKLYLGTATLGEKIPGWSKAGPLEMAQLM 60
Qy 61 ITHFGPEAVRLALSTPERINRDLWERGQEDLVR-----DPQETRYDVVRKKFLME 114
Db 61 VAHGTREAWLLALSTFQRHKKDLWERGQEDLVRGKGGDLQTTKYDYVRKKFLME 120
Qy 115 DRNARLGEVNLSHRYTRLLLVKEHSPMVQVQQLDTRGHARTVGHQASPIKIETLFE 174
Db 121 DRNARLGEVNLNRYTRLLLVKEHSPNPIWQKQFVDEWERSRTRRQTSPIQMELFE 180
Qy 175 PDEERPPRTVMQAGAGICKSLAHKMLMDWADGKLFQGRPDYLYINCREMNSQATE 234
Db 181 PDEERPPPTVVLQAGAGKMSLAHKMLMDWADGRLFGQRFYVYISCRELNRSHQ 240
Qy 235 CSMQDLIFSCWPEPSAPLQELIRVPERLLFTIDGFDELKPSFHPDQGPWCLCWEEKPTE 294
Db 241 CSVDQLISSCWPERGISLEDLMQAPDRLLFTIDGFDLKHSFHDQAQFPCWLCWEEKPTE 300
Qy 295 LLNLSLRKXLLPESLLITRPTALEKHLRLBHPHRLVEILGFSPEARKEYFYKYPHNA 354
Db 301 VLLGSLIRLLLPQVSLITRTPCALEKHLGLLEHPRHVEILGFSPEARKEYFYRYFHT 360
Qy 355 EQAQGVFNRYRDNPEFTMCFVPLVCHVCTCLOQQLGEGGLLRQTRTTAVYMLYLS 414
Db 361 QQASRVLSFLMDYEPFTMCFVPMVSWVCTCLKQQLGEGGLLRQTRTTAVYMYFLLS 420
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Qy 415 LMQPKPGAPRLQPPNQRLGICSLAAGLWLNQKILFEBQDLRKHKGLDGEDVSAFLNMIFQ 474
Db 421 LMQPKPGTPTFKVPANQRLGVLAAEGLWLNQKILFEBQDLRKHKGLDGDVSTFLNMIFQ 480
Qy 475 KDINCERYYSFIHLSFOEPFAAMYIILDEGEAGGPPQDVTRLLTTEYAFSPERSFALTSR 534
Db 481 KGKCKEYFIFHLSFOEPFAAMYIILDEGEAGGPPQDVTRLLTTEYAFSPERSFALTSTV 533
Qy 535 FLFGLLNEETRSHLEKSLCWKSPHPIKMDLLOWTQSKAQSDGSTLQGSLEFFSCLYEIQ 594
Db 534 FLFGLLNEENRCYLERNLGHISIPQVKEEVLANIQWAGSEGSTLQGSLELLSCLYEIQ 593
Qy 595 EEEFIQOALSHFQVIVVSNIASRMEHVMVSFCLKRCRSAQVHLHYGATYSGEDRARCS 654
Db 594 EEDFIQOALSHFQVIVVRSISIKMEHVMVSFCARYCRSTEVHLHGSAYSTGEMDDPPEP 653
Qy 655 AGAHTLLVQLRPRTVLLDAYSEHLAAALCTNPNLIELSLYRNALSGRVKLLCOGLRHP 714
Db 654 SGVQTOSTYLQ-ERNMLPDVYSAYLSAAVCTNSNLIELALYRNALSGQVRLLCQGLRHA 712
Qy 715 NCKLQNL 721
Db 713 SKCLQNL 719

RESULT 3
CIS1_HUMAN STANDARD; PRT; 1034 AA.
ID Q36P20; O75434; Q8TCW0; Q8TEU9; Q8WXH9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cold autoinflammatory syndrome 1 protein (Cryopyrin) (NACHT-, LRR- and
DE PYD-containing protein 3) (PYRIN-containing APAF1-like protein 1)
DE (Angiotensin/vasopressin receptor AII/AVP-like).
GN Name=C1ASI; Synonyms=NALF3, PYPAF1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), VARIANTS FCAS MET-198; VAL-439
RP AND GLY-627, AND VARIANT MWS VAL-352.
RX MEDLINE=21547523; PubMed=11687797; DOI=10.1038/ng756;
RA Hoffman H.M., Mueller J.L., Broide D.H., Wenderer A.A., Kolodner R.D.;
RT "Mutation of a new gene encoding a putative pyrin-like protein causes
RT familial cold autoinflammatory syndrome and Muckle-Wells syndrome.";
RL Nat. Genet. 29:301-305(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=21909508; PubMed=11786556; DOI=10.1074/jbc.M112208200;
RA Manji G.A., Wang L., Geddes B.J., Brown M., Merriam S., Al-Garawi A.,
RA Mak S., Lora J.M., Briskin M., Jurman M., Cao J., Distefano P.S.,
RA Bertin J.;
RT "PYPAF1: a PYRIN-containing APAF1-like protein that assembles with ASC
RT and activates NF-kB.";
RL J. Biol. Chem. 277:11570-11575(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), VARIANT MWS MET-198, AND
RP VARIANTS FCAS/MWS TRP-260 AND PRO-305.
RX MEDLINE=22411234; PubMed=12355493; DOI=10.1002/art.10509;
RA Aganna E., Martinon F., Hawkins P.N., Ross J.B., Swan D.C.,
RA Booth D.R., Lachmann H.J., Gaudet R., Woo P., Feighery C.,
RA Cotter F.E., Thome M., Hitman G.A., Tschopp J., McDermott M.F.;
RT "Association of mutations in the NALP3/C1ASI/PYPAF1 gene with a broad
RT phenotype including recurrent fever, cold sensitivity, sensorineural
RT deafness, and AA amyloidosis.";
RL Arthritis Rheum. 46:2445-2452(2002).
RN [4]
RP SEQUENCE OF 391-1034 FROM N.A. (ISOFORM 1).
RX TISSUE=Umbilical cord blood;
RN MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
```


RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
[5]
RN VARIANT FCAS MET-198, VARIANTS MWS ASN-303; MET-348; THR-439 AND
RN ARG-569, AND VARIANT FCAS MWS TRP-260.
RP MEDLINE=21987640; PubMed=11922256;
RX Dode C., Le Du N., Culisset L., Letourneur F., Berthelot J.-M.,
RA Vaudour G., Meyrier A., Watts R.A., Scott D.G.I., Nicholas A.,
RA Granel B., Frances C., Garcier F., Ederly P., Boulanguet S.,
RA Domergues J.-P., Delpech M., Grateau G.;
RT "New mutations of CIAS1 that are responsible for Muckle-Wells syndrome
RT and familial cold urticaria: a novel mutation underlies both
RT syndromes.";
RL Am. J. Hum. Genet. 70:1498-1506(2002).
[6]
RN VARIANTS CINCA ASN-303; SER-309; ARG-358; ASN-436; SER-573 AND
RN THR-662, AND TISSUE SPECIFICITY.
RX MEDLINE=22062555; PubMed=12032915;
RA Feldmann J., Prieur A.-M., Quartier P., Berquin P., Certain S.,
RA Cortis E., Teillac-Hamel D., Fischer A., de Saint-Basile G.;
RT "Chronic infantile neurological cutaneous and articular syndrome is
RT caused by mutations in CIAS1, a gene highly expressed in
RT polymorphonuclear cells and chondrocytes.";
RL Am. J. Hum. Genet. 71:198-203(2002).
CC -!- FUNCTION: May function as a potential inducer of apoptosis.
CC Interacts selectively with apoptosis-associated specklike protein
CC containing a CARD domain (ASC). This complex may function as an
CC upstream activator of NF-kappa-B signaling.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=2;
CC IsoId=Q96P20-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q96P20-2; Sequence=VSP_005520, VSP_005521;
CC Name=3;
CC IsoId=Q96P20-3; Sequence=VSP_005519;
CC TISSUE SPECIFICITY: Expressed in blood leukocytes. Strongly
CC expressed in polymorphonuclear cells, undetectable or expressed
CC at a lower magnitude in B and T lymphoblasts, respectively. High
CC level of expression detected in chondrocytes. Low or no expression
CC in the other tissues tested.
CC -!- DISEASE: Defects in CIAS1 are a cause of familial cold
CC autoinflammatory syndrome (FCAS) [MIM:120100]; commonly known as
CC familial cold urticaria. FCAS is rare autosomal dominant systemic
CC inflammatory disease characterized by episodes of rash,
CC arthralgia, fever and conjunctivitis after generalized exposure to
CC cold.
CC -!- DISEASE: Defects in CIAS1 are a cause of Muckle-Wells syndrome
CC (MWS) [MIM:191900]; a rare autosomal dominant fever syndrome with
CC episodic urticaria, arthralgia, amyloidosis and progressive
CC sensorineural deafness.
CC -!- DISEASE: Defects in CIAS1 are the cause of chronic infantile
CC neurologic cutaneous and articular syndrome (CINCA) [MIM:607115];
CC also known as 'neonatal onset multisystem inflammatory disease',
CC or NOMID, a rare congenital inflammatory disorder characterized by
CC a triad of neonatal onset of cutaneous symptoms, chronic
CC meningitis, and joint manifestations with recurrent fever and
CC inflammation.
CC -!- SIMILARITY: Contains 1 DAPIN domain.
CC -!- SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
CC -!- SIMILARITY: Contains 1 NACHT domain.
CC -!- CAUTION: Ref.4 sequence differs from that shown due to frameshifts
CC in positions 893, 918 and 926.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF410477; AAL33908.1; -;
DR EMBL; AF427617; AAL33911.1; -;
DR EMBL; AY051117; AAL12497.1; -;
DR EMBL; AY051112; AAL12497.1; JOINED.
DR EMBL; AY051113; AAL12497.1; JOINED.
DR EMBL; AY051114; AAL12497.1; JOINED.
DR EMBL; AY051115; AAL12497.1; JOINED.
DR EMBL; AY051116; AAL12497.1; JOINED.
DR EMBL; AY056059; AAL12497.1; JOINED.
DR EMBL; AY056060; AAL12497.1; JOINED.
DR EMBL; AY051117; AAL12498.1; -;
DR EMBL; AY051112; AAL12498.1; JOINED.
DR EMBL; AY051113; AAL12498.1; JOINED.
DR EMBL; AY051114; AAL12498.1; JOINED.
DR EMBL; AY051115; AAL12498.1; JOINED.
DR EMBL; AY051116; AAL12498.1; JOINED.
DR EMBL; AF420469; AAL65136.1; -;
DR EMBL; AF468522; AAL78632.1; ALT_INIT.
DR EMBL; AY092033; AAM14669.1; ALT_INIT.
DR EMBL; AF418985; AAL14640.2; ALT_INIT.
DR EMBL; AF054176; AAC39910.1; ALT_FRAME.
DR HSP; P10775; 2BNH.
DR Genew; HGNC:16400; CIAS1.
DR MIM; 606416; -;
DR MIM; 120100; -;
DR MIM; 191900; -;
DR MIM; 607115; -;
DR GO; GO:0006917; P:induction of apoptosis; NAS.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0007165; P:signal transduction; NAS.
DR InterPro; IPR001611; LRR_RNinh.
DR InterPro; IPR007091; LRR_RNinh_sub.
DR InterPro; IPR003590; LRR_RNinh_sub.
DR InterPro; IPR007111; NACHT_NTPase.
DR InterPro; IPR004020; PAAD_DAPIN.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF05729; NACHT; 1.
DR Pfam; PF02758; PAAD_DAPIN; 1.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00368; LRR_RI; 3.
DR PROSITE; PS00824; DAPIN; 1.
DR PROSITE; PS00837; NACHT; 1.
KW Alternative splicing; Apoptosis; Deafness; Disease mutation;
KW Leucine-rich repeat; Repeat.
FT DOMAIN 1 91 DAPIN.
FT DOMAIN 218 534 NACHT.
FT REPEAT 738 761 LRR 1.
FT REPEAT 795 818 LRR 2.
FT REPEAT 852 875 LRR 3.
FT REPEAT 881 904 LRR 4.
FT REPEAT 909 937 LRR 5.
FT REPEAT 939 961 LRR 6.
FT REPEAT 966 989 LRR 7.
FT DOMAIN 688 695 Poly-Glu.
FT VARSPLIC 718 1034 Missing (in isoform 3).
FT VARSPLIC 719 775 Missing (in isoform 1).
FT VARSPLIC 834 890 Missing (in isoform 1).
FT VARSPLIC 198 198 V -> M (in FCAS and MWS).
FT VARSPLIC 260 260 R -> W (in FCAS and MWS).
FT VARSPLIC 303 303 D -> N (in CINCA and MWS).
FT VARSPLIC 305 305 L -> P (in FCAS and MWS).
FT VARSPLIC 309 309 F -> S (in CINCA).

FT VARIANT 348 348 /FTid=VAR_014106.
 FT T -> M (in MMS).
 FT /FTid=VAR_014366.
 FT A -> V (in MMS).
 FT /FTid=VAR_013228.
 FT H -> R (in CINCA).
 FT /FTid=VAR_014367.
 FT T -> N (in CINCA).
 FT /FTid=VAR_014368.

Query Match 43.8%; Score 2396; DB 1; Length 1034;
 Best Local Similarity 46.18; Pred. No. 1.1e-161;
 Matches 495; Conservative 175; Mismatches 303; Indels 100; Gaps 10;

QY 11 CRISTYLEEELAEVLEKFKLYL-GTATELGEGKIPWGSMEKAGPLEMAQLLTHFGPEEA 69
 DB 6 CKLARYLEDLEDVLDKFKFMLEDPYPPKGCIPLPGRQTEKADHVDLATLMDFNGBKA 65

QY 70 WRLALSTFERINRDKLWEGQRED----- 93
 DB 66 WAMAVWTFIAINRRDLYEKARDEPKWGSNARVSNPTVICQEDSIEEEMWGLLEYLSRI 125

QY 94 ----LVDPDPOETVRYRRFRLEMDERNARIGECVNLSHRYTRLLLVKEHSPNQVQOOL 149
 DB 126 SICWKKDYRKRYKRYRSFQCIEDNRALGESVSLNKRYTRLRIKEHRSQOEREQL 185

QY 150 LDTGRGHARTVGHQASPIKTIETPEDEERPEPPTVVMQAGAGIKSMIAHKVMDLWAD 209
 DB 186 LAIGK--TKCESPVSPKIMELLFDPDDEHSEPVHTVVFQAGIGKTIARXKMLDNAS 243

QY 210 GKLFQGRFDYLYINCREMNSQATECSMDQLIFSCWPEPSAPIQELIRVPERLLFIIDGF 269
 DB 244 GTLYQDRFDYLYVTHCREVS-LVTRQSLGDLINSCCPDPNPIHKIVRKPSRILFLMDGF 302

QY 270 DELKPSFHDQGPWCLWEKRPTELALNSLRKLPAPLPELSLITPTALEKHLRLLEH 329
 DB 303 DELQAFDEHIGPLCTDQKAEGRDILLSLRKLKLPPEASLITTPVALEKHLQLLHD 362

QY 330 PRHVEILGFSEARKEYFYKYFHNAEQAGQVFNVRDNEPLFTMCFVPLVCVVCTCLOQ 389
 DB 363 PRHVEILGFSEARKEYFYKYFDEQAQAAAFSLIQENEVLFTMCFPIPLVCMVCTGLKQ 422

QY 390 QLEGGLLRQTSRTTAVMYLILSLMQPKGAPRLQPPNQKGLCSLAADGLWNOKILF 449
 DB 423 QMESGKSLAOTSKTITAVYVFFLSLLQPRGSGQEHGLCAHLWGLCSLAADGIWNOKILF 482

QY 450 BEODLRKHGIDGEDVSAFLNMNIFQDINCERYYSRTHLSFQFEFAAMYILDEGGAG 509
 DB 483 EESDLRNLHGQKADVSAFLNMNIFQKEVCEKFSYFIHMTFQBFPAAMYLLBEEKEGRT 542

QY 510 -----PDQDVTRLLTYAFSERSFLALTSRFLFGLNNEETRSKLSKWCWKSPIHI 560
 DB 543 NVFGSRLLKPSRDVTVLLENYGRFEKGYLIFVVRFLFGLVQNETSVLEKLSCKLSQOI 602

QY 561 KMOLLQWISQASGDSTLQOGSLFPPSYLYEQEEFIQOALSHFOVIVVSNIAKMEH 620
 DB 603 RLELLKWEIVKAKAKKIQIOPSQLELPYLYEQEEDFQVAMDYPPKIEI-NLSTRMDH 661

QY 621 MVSSPCLKRCESQAQVHLHYNTASDGEDRARCAGATILLVQLRPRTVLLDAYSEHLA 680
 DB 662 MVSSFCIENCHRVESLSL-GFLNMKPEEEEEKEGRHLDVQ----- 703

QY 681 AALCTNPNTIELSLRYNALSGRVKLLCQGLRHPNCKLQNLRLKRCRISSSACEDLSAAL 740
 DB 704 ---CVLPS-----SSHAACSHG-----LVNSHLTSSFCRGLFSVL 735

QY 741 IANKNLTRMDLSNGVGFPGMILLCEGLRHPQCRLOMIQRKQLESGACQEMASVLGTN 800
 DB 736 STQSRLTELDLSNLSLGDPMGVLCETLQHPGCMIRRLWLRGRCLSHECCFDLSVLSSN 795

QY 801 PHLVELDLTGNALEDGLRLILCOGLRHPVCLRLTLWLKICRLTAACADELASTLSVNOQL 860
 DB 796 QKLVELDLSNALGDGFGIRLLCVGLKHLKLLCNLKLVLVSCCLTSACCQDLASVLSHSL 855

QY 861 REIDLSLNEIGDGLVLLLCGLRHPTCKLQTLRLIGICRLGSAACEGLSVVLQANHNLREL 920
 DB 856 TRLYVGENALGDSGVAILCEKAKNPQCNKQKGLVNSGLTSVCCSALSLSVLSTNQLTHL 915

QY 921 DLSFNLDGLDWGLWLLAEGLOHPACRLOKQLWLDSCGLTAKACENLYFTLGINOTLDTLYLT 980
 DB 916 YLRGNTLGDGKIGKLLCEGLLHPDKLQVLELDNCLNTHSCCWDLSTLLTSQSRLKLSLG 975

QY 981 NNALGDTGVRLLCRLSHPGCKLRVLWLFQMDLNKMTHTSRLAALRVTKPVLDI 1033
 DB 976 NNDLGLDGVMMFEVLKQQSCLLQNLGLSEMYFNYSKSALETLOEBKPELTV 1028

RESULT 4

CISI_MOUSE
 ID CIS1_MOUSE STANDARD; PRT; 1033 AA.
 AC QBR4B8;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cold autoimmune syndrome 1 protein homolog (PYRIN-containing
 DE APAF1-like protein 1) (Mast cell maturation inducible protein 1).
 DE Names-Cisai; Synonyms=Mmigl, NALP3, Pypafi;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=BALB/cJ;
 RA Kikuchi-Yanoshita R., Koga K., Taketomi Y., Sugiki T., Saito T.,
 RA Ishii S., Hisada M., Suzuki-Nishimura T., Uchida M.K., Moon T.-C.,
 RA Chang H.-W., Sawada M., Inagaki N., Nagai H., Murakami M., Kudo I.;
 RT "Identification of inducible genes during in vitro maturation of mouse
 RT bone marrow-derived mast cells to connective tissue-type mast cells.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May function as a potential inducer of apoptosis.
 CC INTERACTS selectively with apoptosis-associated specklike protein
 CC containing a CARD domain (ASC). This complex may function as an
 CC upstream activator of NF-kappa-B signaling (By similarity).
 CC -1- SIMILARITY: Contains 1 DAPIN domain.
 CC -1- SIMILARITY: Contains 7 leucine-rich
 CC -1- SIMILARITY: Contains 1 NACHT domain.
 CC -----
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EMBL; AF486632; ALA090874.1; -;
 DR HSSP; P10775; 2BNH.
 DR MGD; MGI:2653833; C1a1.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007091; LRR_Nrnh.
 DR InterPro; IPR007111; NACHT_NTPase.
 DR InterPro; IPR004020; PAAD_DAPIN.
 DR Pfam; PF00560; LRR; 6.
 DR Pfam; PF05729; NACHT; 1.
 DR Pfam; PF02758; PAAD_DAPIN; 1.
 DR PRINTS; PR00019; LEURICHPPT.
 DR PROSITE; PS50824; DAPIN; 1.
 DR PROSITE; PS50837; NACHT; 1.
 DR Apoptosis; Leucine-rich repeat; Repeat.
 KW Apoptosis; Leucine-rich repeat; Repeat.
 FT DOMAIN 1 91
 FT DAPIN.
 FT 216 532
 FT NACHT.
 FT 737 760
 FT LRR 1.
 FT REPEAT 794 817
 FT LRR 2.
 FT REPEAT 851 874
 FT LRR 3.
 FT REPEAT 880 903
 FT LRR 4.

[illegible]

Db 363 PRHVEILGFSAKREYFFKFSDEAQAARAFSLIQENEVLFTWCFPLVCWIVCTGLKQ 422
Qy 390 QLEGGGLLROTSRTTAYVYLLSLMOPKPGAPLPPPNORGLCSLAADGLNQNKLIF 449
Db 423 QMESGKSLAQTSKTTAYVYFLLSLQPGSGQEHGLCAHLWGLCSLAADGIWNQKILP 482
Qy 450 EQDLRKHGLDGEVSAFLNWNIFQKINCIBRYYSFIHLSQEPFAAMYILDEGEAG 509
Db 483 EESDLRNLHGLQADVASAFRLNLPQKEDCEKFSFIHMTFOEFFAAMYLLBEKEGRT 542
Qy 510 -----PDODYTRLLTEAFASERSFLATSLPFLGLNEETRSHEKSLCWKVSPI 560
Db 543 NVPSRLKPSRDVTLLENYKPEKGYLFPVRFGLVNOERTSYLEKSLCKISQOI 602
Qy 561 KMDLLQWTSQAQSGDSTLQOGSLEFFSCSYEIEQEEFIQOALSHFOVIVVSNIASQWEH 620
Db 603 RLELLKWEVKAQAKKQIQPSQLEFLCYLMEDEDFVQAMDYFPKIEI-NLSTRMDH 661
Qy 621 MVSSFCLKRCRSAOVHLHYGATYSGADGEDRARCAGAHLLVQLRPBTVLLDAYSHLA 680
Db 662 MVSSFCIENCHRVESLSL-GFLHNPKEEBEKEGRHLDVQ----- 703
Qy 681 AALCTNPNLIELSLYRNALSGRVKLLCOGLRHFNCKLQNLRLKRCRISSACEDLSAAL 740
Db 704 ---CVLPS-----SSHAAC----- 714
Qy 741 IANKNLTRMDLSGNGVFGPGMMLCEGLRHFPQCRLOQLRKCGLSCGAGQOEMSVLGTN 800
Db 715 -----SGLG-----RCGLSHECCFDLSVLSSN 738
Qy 801 PHVELDLTGNALEDGLRLCCOGLRHFPVCRRLTLWLKICRLTAACDELASTLVNQSL 860
Db 739 QKVELDLSNALGDFGRLLCVGLKLLCNLKLWLVSCLTSACQDLASVLSTSHSL 798
Qy 861 RELDLSNELDGLVLLCEGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHLREL 920
Db 799 TRLYVGENALGDSGVAITCEKAKNPQCNLQKLGIVNSGLTSVCCSALSLSVLTQNLTHL 858
Qy 921 DLSFNDLGDWGLWLLAEGLOHPACRLQKLDSDGLTAKACENLYFTLGINOTLTDLYLT 980
Db 859 YLRGNTLGDGKILKCEGLLHPDCKLQVLELDNCLNLSHCCWDLSTLTSQSQRKLSLG 918
Qy 981 NNALGDTGVRLLCRLSHPGCKRLVWLFGMDLNMKTHSLAALRVTKPYLDI 1033
Db 919 NNDLGLGVMMFCEVLKQOSCLLQNLGSEMYFNYETKSALETQEEKPELTV 971

RESULT 6

NA14 HUMAN STANDARD; PRT; 1093 AA.
ID NA14 HUMAN Q86W24; OTRR6;
AC Q86W24; OTRR6;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE NACHT-, LRR- and PYD-containing protein 14 (Nucleotide-binding oligomerization domain protein 5).
GN Name=NA14; Synonyms=NODs;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22451042; PubMed=12563287; DOI=10.1038/nrml1019;
RA Tschopp J., Martinon F., Burns K.;
RT "NALP3, a novel protein family involved in inflammation."; Nat. Rev. Mol. Cell Biol. 4:95-104(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22651535; PubMed=12766759; DOI=10.1038/nrml1086;
RA Inohara N., Nunez G.;
RT "NODs: intracellular proteins involved in inflammation and

RT apoptosis.";
RL Nat. Rev. Immunol. 3:371-382(2003).
CC -|- FUNCTION: Involved in inflammation (Potential).
CC -|- SIMILARITY: Contains 1 DAPIN domain.
CC -|- SIMILARITY: Contains 11 leucine-rich (LRR) repeats.
CC -|- SIMILARITY: Contains 1 NACHT domain.
CC -----
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CC -----
DR EMBL; AY154469; AA018165.1; -.
DR EMBL; BK001107; DAA01240.1; -.
DR HSPSP; P10775; 2BNH.
DR Genew; HGNC:22939; NALP14.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007091; LRR_RNinh.
DR InterPro; IPR007111; NACHT_NTPase.
DR InterPro; IPR004020; PAAD_DAPIN.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF05729; NACHT; 1.
DR Pfam; PF02758; PAAD_DAPIN; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR PROSITE; PS00824; DAPIN; 1.
DR PROSITE; PS00837; NACHT; 1.
DR ATP-binding; Leucine-rich repeat; Repeat.
KW DOMAIN 1 97 DAPIN.
FT DOMAIN 177 499 NACHT.
FT REPEAT 525 550 LRR 1.
FT REPEAT 672 695 LRR 2.
FT REPEAT 733 756 LRR 3.
FT REPEAT 757 780 LRR 4.
FT REPEAT 785 807 LRR 5.
FT REPEAT 842 869 LRR 6.
FT REPEAT 871 894 LRR 7.
FT REPEAT 899 926 LRR 8.
FT REPEAT 956 979 LRR 9.
FT REPEAT 985 1008 LRR 10.
FT REPEAT 1013 1037 LRR 11.
SQ SEQUENCE 1093 AA; 124732 MW; 124EEACE22A11D6F CRC64;
Query Match 32.9%; Score 1799; DB 1; Length 1093;
Best Local Similarity 37.4%; Pred. No. 4e-119;
Matches 413; Conservative 177; Mismatches 388; Indels 126; Gaps 15;
Qy 13 LSTYLBEELEAVELEKFKLYLGTATLGEKIPWGSMEKAGPFLMAQLLTHFGPPEAWRL 72
Db 15 LLLYLBELNKEELNTFKLFLKETMEPEHGLTPNNEVKARREDLANLKKYYPGEKASV 74
Qy 73 ALSTFERINKDLWEGQRE-----DLVRDPQET-----YRDYVRRKF 110
Db 75 SLKIFGKMLKDLCEKAKEINNSAQTIGPDDAKAGETQDQBAVLGDGTEYRNRIKEKF 134
Qy 111 RLMDERNARLGEVCNLSHRYTRLLLVKHSNPNQVQQQLDTCGHARTVGHQASPIKIE 170
Db 135 CITWKKSLAGKPEDFHG-----YAKDKRL-----LE 163
Qy 171 TLPEDEERPEPRTPVVMQGAAGIKGSMIAHVKMLDQWADKGLFGFRDYLYFNCREMNQ 230
Db 164 HLFVDVKTGAQFIQVVLQGAAGVGTLLVRKAMLDWAGSLYQQRKYFYVLYNGRINQ 223
Qy 231 SATECSNQDLIFSCWPSPSAPLOELIRVPERLLFIIDGFDLKPSPHDPQGMCLCWEK 290
Db 224 -LKERSFAQLISKDWPSTEGPIEIMVQPSLLFIIDSFDLNPFAPEPEFALCEDWTQE 282
Qy 291 RPTPELLNSLRKLLPELSLLITTPALEKLRHLEHPRHVEILGFSAEKREYFYKY 350
Db 283 HPVSFLMSSLLRKVMLEASLLVTRTLTTSKRLKQLKNNHYVELLGMSEDAEEYIQF 342

-!- MISCELLANEOUS: The sequence shown here is derived from an entry /GorBank/0001 third party annotation (TPA) entry.

351 FHNAEQRAGQVFNYYVRDNEPFLTMCFVLVWVCTCLOOQLGEGGLLRQTSRTTAYTML 410
 :
 343 FEDKRWAMKVFSLLSKNEMLP SMCQVPLVCWAACATCLKQQMEKGDDVTLTCTTTALFTC 402
 :
 411 YLLSLMQP-KGCAPLQP PPNQ--RGICSLAADGLWNOKILFBEQDLRKHGLGDGEDYSA 466
 :
 403 VISSLFTPVDDGSPSL---PQAQLRLRCQVAAKGIWTMTVVFRENRLRLGLTCSDVSS 459
 :
 467 FLNNMIFOKINCERYYSFIHLSPFOEPFAAMYIL----DSGEGAGGPDPQDVTRILLTYA 522
 :
 460 FWDSNIOKDABEYENCYVFTLHVGEFPAAMPYMLKGSWEAGNPSCPFEDLKSLQSTS 519
 :
 523 PSERSFLALTSRPIECIANEEETRSHLEKSLCWKVSPIHKMDLLOWIOSKAOSDGSTLQOG 582
 :
 520 YKD-PHLTQMCKFLFGLLNEDRVKLERTFNCMSBLKISKLLQCMVEVLGNSDYSPSQLG 578
 :
 583 SLPEFSCLYEIIEEFBFIQALSHFQIVVVSNTASKMEHVMVSFCUKRCRSAQVLHYGA- 641
 :
 579 FLELPHCLYEYTDKAFISQAMRCFPKVAI-NICEKIHLVVSSFCLKHCRCLFRTIRLSVTV 637
 :
 642 -----TYSADGEDRARC-----SAGAHTLLVQLRPERTVLLDAYSEHL----- 679
 :
 638 VFEKKILTSLPTNTWDGRITHCWODLCSVLHT-----NEHLRELDLYHSNLDKSAMN 691
 :
 680 -----AAAACTNPNI.IELSLRYRNALGRSGVKLLCQ 709
 :
 692 ILHHELRHPNCKLQKLKLFITPPDCQDISTLIHKNLMHLDLKGSDIGNGVKSLCE 751
 :
 710 GLRHPNCKLONRLKRCRISSACEDLSAALTANKULTRMDSLGNVGVPFGHMLLCEGLR 769
 :
 752 ALKHPECKLQTLRESCNITVFCLINSNALRSQSILI.FLINSTNNLLDDGVQLLCEALR 811
 :
 770 HPCRLQMTOLRKCOLLESACQSMASVLGTNP.HLVELDITGNALEDGLRLLCQGLRHVP 829
 :
 812 HPKCYLERLSLESCGLTEACGEVLSIALINSKRLTHLCDNVLDGGVKLMSDALQHAQ 871
 :
 830 CRURTWLTKCRUTAAACDELASTLSVNQSLRELDLSINELGDLGVLLCGELRHPTCKL 889
 :
 872 CTLKSLVLRCHFTLSISEYLSLSLHNKS.LTHLDLGSNWLDQNGVKLLCDVFRHPSCNL 931
 :
 890 QTLRLGICRLGSAACEGLSVVLQANHNLRDEL.SFNDLGDWGLWLWLAEGI.QHPACRLQKL 949
 :
 932 QDELMECVLTNACCLDLASVILNNPNRLSLDIGNNDLQDDGVKILCDALRYFNCNIQRL 991
 :
 950 WLBSOGLTKACENLYETLGINQTLDLYLTNNALGDTGVRL.CKLSHPGCKLRVLWLF 1009
 :
 992 GLEYCGLTSLCCDDSSALICNKRLIKONLTQNTLVGYEGIVKLYKVLKSPCKLQVLGLC 1051
 :
 1010 GMDLNKMKTHSLAALRVTKPVDI 1033
 :
 1052 KEAPDEEAQKLEAVGVS.NPHLI 1075
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 RESULT 7
 Q7RTR0 PRELIMINARY; PRT; 991 AA.
 AC Q7RTR0;
 DT 01-MAR-2004 (TremBLrel. 26, Created)
 DT 01-MAR-2004 (TremBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
 DE N006.
 GN Name=N006;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22651535; PubMed=12766759;
 RA Inohara N., Nunez G.;
 RT "NODs": Intracellular proteins involved in inflammation and apoptosis.";
 PL Nat. Rev. Immunol. 3:371-382(2003).


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Qy 782 KQLESGACQEMASVLTGNPHLVLDLTGNALDGLRLQLCOGLRHPVCRRLTLWLKICR 841
Db 723 KCDISSEVCEDIASVLACNSKHLKLSLVENPLRDEGMTLLCEALKSHCALERLMLVYC 782
Qy 842 LTAACDELASTLSVNQSLRELDLSNELDGLVLLCEGLRHPTCKLQTLRLGICRLGS 901
Db 783 LTSVSCDSISEVLLCSLSLDDLSGNALEDNGVASLCAALKHPGCSIRELWLMGCFITS 842
Qy 902 AACBGLSVVLQANHLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKLWLDSCGLTAKAC 961
Db 843 DSKCDIAAVALICNGKLTGLKHNIEIGDTGVRLCAALQHPCKLECLGLQTCPIRACC 902
Qy 962 ENLYFTLGINQTLTDLVLTNNALGDTGVRLCKRLSHPGCKRLVLMFGMDLNRQTHSRL 1021
Db 903 DDIAAALIACTLRSLNLDWIALDADAVVVLCEALSHDPDCALQMLGLHKSFGDEETKIL 962
Qy 1022 AALRVTKPYLDI 1033
Db 963 MSVEKIPHLTI 974

RESULT 8
ID Q86W27 PRELIMINARY; PRT; 986 AA.
AC Q86W27;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE NALP9
GN Name=NALP9;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22451042; PubMed=12563287;
RA Tschopp J., Martinon F., Burns K.;
RT "NALPs: a novel protein family involved in inflammation.";
RL Nat. Rev. Mol. Cell Biol. 4:95-104(2003).
DR EMBL; AY154464; AA018160.1; -.
DR HSSP; P10775; 2BNH.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007091; LRR_RNinh.
DR InterPro; IPR007111; NACHT_NTPase.
DR InterPro; IPR004020; PAAD_DAPIN.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00560; LRR_1; 4.
DR Pfam; PF05729; NACHT; 1.
DR Pfam; PF02758; PAAD_DAPIN; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS0824; DAPIN; 1.
DR PROSITE; PS0837; NACHT; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
SQ SEQUENCE 986 AA; 112592 MW; B4248B46F70413B2 CRC64;

Query Match 27.5%; Score 1505.5; DB 2; Length 986;
Best Local Similarity 34.2%; Pred. No. 2.9e-98;
Matches 344; Conservative 193; Mismatches 383; Indels 85; Gaps 18;

Qy 16 YLELEAVELEKFKLYLGTATLECEGK-IPGSMKEKAGPLEMAQLLITHFGEAWRLAL 74
Db 14 YLKLREEFWKFKELKQLKPLEKELKPIPAWELKKASKEDVAKLLDKHVGKQAWETL 73
Qy 75 STFERINRKLWEGQREDLVDPQETTYRVDYVRKFRIMEDNRNARLGEVGNLSHRYTRL 134
Db 74 NLFQINRKLWLWKAQEE--MRNKLNPYRKHKMTFQLWEKET---CLHVPHEFYKET 127
Qy 135 LVKESHPMQVQQLDTGTRGHARTVGHQASPIKIELTFEPDEPERPPRTVVMQGAAGI 194
Db 128 MKNEY-----KELNDAYTAARR-----HTVVLGEGDGI 156

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Qy 195 GKSLAHKVMLDWADGKLFQGRFDYFYINCREMNOGATECSMODLIFSCWPBPSAPLOQ 254
Db 157 GKTTLLRKVMDWAEGNLWKDRFTFFVFLNVCEMNGIA-ETSLLELLSRDWPESSEKIED 215
Qy 255 LIRVPERLLFIIDGFD-----ELKPSFHPDQPGPWCWCKWEKRTPELLLSLIRKLLPE 308
Db 216 IFSQPERILFIMDGFQELKFNQLKADLSD-----WRQRPMPILTSLLQKGMLE 268
Qy 309 LSLITTRPTALEKHLLEHPRHVEITLGFSEAEKKEYFYKYPHNAQAGOVFNVDNE 368
Db 269 SLLIALGKLMQKHYPMLRHPKLIKULGFSESEKSYFYFFGGEKSKALKVFNVRDNG 328
Qy 369 PLFTMCVPVPLVWVCTCLOQOEGGGLRQTSRTTTAVTMYLLSLLMQPKPGAPRLQPP 428
Db 329 PLFTLCHNPFTCMVCTCVKQRLGERGDLINSQNTTYLYASFLTYV--KAGSQSPFK 386
Qy 429 PNQ---RGLCSLAADGLWNQKILFEEQDLRKHLGDGEDVSAFLNMNIFQKDINCERYSP 485
Db 387 VNRARLKSALAAEGITTYTFVSHGDLRRNGLSESEGVMMVGMRLLRGGDC---PAF 443
Qy 486 IHLSPQEFFAAMYVILDEGEGGAGPD-QDVTRLLITEYAFSERSFLATLSRFLGLLNEET 544
Db 444 MHLICIEFCAMFYLLKRPKDDPNPAIGSITQLVRASVQPTLLTQVGIFMFGISTEEI 503
Qy 545 RSHLEKSLCWKSPHIKMDLLQIQSKAQSDGSTLOQGSLEFFSCLYEIOEEEFIOQALS 604
Db 504 VSMLETSFGFPLSKDLKQEIQTCLLESLSQCEADREATAFOELFGLFETQKEFVTKVMN 563
Qy 605 HFQ--VIVVSNIASQMEHMV--SSFCLKRCRSQVHLHYGATYSADGEDRARCAGAHULL 661
Db 564 FPEVEFYIGNI---EHLVIASFCLKHCQHLTLTRMCVENIFPDD---SGCISDYNEKL 616
Qy 662 VOLRPERTVLLDAYSEHLAALCTNPNIELSLYRNALSGRGVKLLCOGLRHPNCKLQNL 721
Db 617 V-----YRELCSMFTTNKNFQILDMENTSLLDDPSLAILCKALQAPVCKLRKL 664
Qy 722 RLKCRIRISSACEDLSAALIANKNLITRMDLSGNGVGPFGNMMLCEGLRHPCRLQMLQLR 781
Db 665 IPTSVYFGHDS--ELFKAVLHNPHLKLLSLVGTSLQSQSDIRHLCETLKHPMKIEELILG 722
Qy 782 KQLESGACQEMASVLTGNPHLVLDLTGNALDGLRLQLCOGLRHPVCRRLTLWLKICR 841
Db 723 KCDISSEVCEDIASVLACNSKHLKLSLVENPLRDEGMTLLCEALKSHCALERLMLVYC 782
Qy 842 LTAACDELASTLSVNQSLRELDLSNELDGLVLLCEGLRHPTCKLQTLRLGICRLGS 901
Db 783 LTSVSCDSISEVLLCSLSLDDLSGNALEDNGVASLCAALKHPGCSIRELWLMGCFITS 842
Qy 902 AACBGLSVVLQANHLRELDLSFNDLGDWGLWLLAEGLOHPACRLQKLWLDSCGLTAKAC 961
Db 843 DSKCDIAAVALICNGKLTGLKHNIEIGDTGVRLCAALQHPCKLECLGLQTCPIRACC 902
Qy 962 ENLYFTLGINQTLTDLVLTNNALGDTGVRLCKRLSHPGCKRLVLMFGMDLNRQTHSRL 1006
Db 903 DDIAAALIACTLRSLNLDWIALDADAVVVLCEALSHDPDCALQML 947

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RESULT 9
Q68U61
ID Q68U61 PRELIMINARY; PRT; 506 AA.
AC Q68U61;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Cryopyrin (Fragment).
GN Name=CIAS1;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.

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RX PubMed=15302403; DOI=10.1016/j.gene.2004.05.002;
RA Anderson J.P., Mueller J.D., Rosengren S., Boyle D.L., Schaner P.,
RA Cannon S.B., Goodyear C.S., Hoffman H.M.;
RT "Structural, expression, and evolutionary analysis of mouse CIAS1.";
RL Gene 338:25-34(2004).
DR EMBL: AY338196; AAR03565.1; -.
DR InterPro: IPR007111; NACHT_NTPase.
DR Pfam: PF05729; NACHT, 1.
DR PROSITE: PS50837; NACHT, 1.
FT NON_TER 1
FT NON_TER 506
FT SEQUENCE 506 AA; 58685 MW; BAA2A16BD583CAE4 CRC64;
SQ
Query Match 27.3%; Score 1493.5; DB 2; Length 506;
Best Local Similarity 55.3%; Pred. No. 8.4e-98;
Matches 281; Conservative 97; Mismatches 117; Indels 13; Gaps 4;
QY 132 RLLLVKHSNPMQVQQQLDTCGRHARTVGHQAQSPKIETLFFPDEERPEPPRTVMVQGA 191
Db 1 RRLVKEHRSQOEREHELLAIGK--TKTLESPVPIKWEMLFPDDHESEPHVTVVQGA 58
QY 192 AGIGKSMIAHKVMDWADGKLFQGRFDYLFYINCRMNQSAATSCSMQDLIFSCWPEPSAP 251
Db 59 AGIGKTLARKIMLDWASGTLYQDRFDYLFYIHCREVS-LVTQSLGDLIVSCCPDPNPP 117
QY 252 LOELIRVPERLLFIIDGDELKPSFHDQPGWCLWEEKRPTTELLNSLRKLLPELSL 311
Db 118 IHKIVRKPRIILFMDGDFDELQAFDEHIGPLCTDWQKAERGDIILSSLRKLLPEASL 177
QY 312 LITRPTALEKHLRLLHPHVEILGFSEARKEYFYKYFHNAEQAGQVFNVRDNEPLF 371
Db 178 LITRPALEKHLHLLDHPHVEILGFSEARKEYFYKYFHNAEQAGQVFNVRDNEPLF 237
QY 372 TMCVPLVWVCTCLOQQLGEGGLLQTSRTTAVYMLYLLSLMOPKPGAPRLQPPNQ 431
Db 238 TMCVPLVWVCTGLKQMESGKSLAQTSTTTAVYVFFLSLLQPRGGSQEHRLCAHL 297
QY 432 RGLCSLAADGLWNQKILFEEDLRKHGLDGEVSFAFLNMI FOKINCERYYSFIHLSFQ 491
Db 298 WGLCSLAADGIWNQKILFEESDLRNHGLQKADVSFAFLNMLFQKEDVCEKFIYFIHMTFQ 357
QY 492 EFFAAMYIILDEGGAG-----PDQDVTRLLTEYAFSERSFIALTSRFLGLNNE 542
Db 358 EFFAAMYILLEEKERRTNIPGSRLLKPSRDVTVLLENYKFKGYLIFVVRFLGLVNG 417
QY 543 ETRSHLEKSLCWKSPHIMDLLOWIQSKAQSDGSTLQOQSLEFPSCLYIEQEEFTQQA 602
Db 418 ERTSYLEKSLCKISQIRLELLKWEVAKAKKLIQPSQLELFYCLYEMQEEDFVQRA 477
QY 603 LSHFQVIVVSNIAKMEHVMVSSFCCLKRC 630
Db 478 MDYFPKIEI-NLSTRMDHVSVSFCIENC 504
RESULT 10
Q68U59 PRELIMINARY; PRT; 506 AA.
ID Q68U59
AC Q68U59;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Cryopyrin (Fragment).
GN Name=CIAS1;
OS Macaca sylvanus (Barbary ape).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9546;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302403; DOI=10.1016/j.gene.2004.05.002;
RA Anderson J.P., Mueller J.D., Rosengren S., Boyle D.L., Schaner P.,
RA Cannon S.B., Goodyear C.S., Hoffman H.M.;
RT "Structural, expression, and evolutionary analysis of mouse CIAS1.";
RL Gene 338:25-34(2004).
DR EMBL: AY338196; AAR03565.1; -.
DR InterPro: IPR007111; NACHT_NTPase.
DR Pfam: PF05729; NACHT, 1.
DR PROSITE: PS50837; NACHT, 1.
FT NON_TER 1
FT NON_TER 506
FT SEQUENCE 506 AA; 58685 MW; BAA2A16BD583CAE4 CRC64;
SQ
Query Match 27.3%; Score 1493.5; DB 2; Length 506;
Best Local Similarity 55.3%; Pred. No. 8.4e-98;
Matches 281; Conservative 97; Mismatches 117; Indels 13; Gaps 4;
QY 132 RLLLVKHSNPMQVQQQLDTCGRHARTVGHQAQSPKIETLFFPDEERPEPPRTVMVQGA 191
Db 1 RRLVKEHRSQOEREHELLAIGK--TKTLESPVPIKWEMLFPDDHESEPHVTVVQGA 58
QY 192 AGIGKSMIAHKVMDWADGKLFQGRFDYLFYINCRMNQSAATSCSMQDLIFSCWPEPSAP 251
Db 59 AGIGKTLARKIMLDWASGTLYQDRFDYLFYIHCREVS-LVTQSLGDLIVSCCPDPNPP 117
QY 252 LOELIRVPERLLFIIDGDELKPSFHDQPGWCLWEEKRPTTELLNSLRKLLPELSL 311
Db 118 IHKIVRKPRIILFMDGDFDELQAFDEHIGPLCTDWQKAERGDIILSSLRKLLPEASL 177
QY 312 LITRPTALEKHLRLLHPHVEILGFSEARKEYFYKYFHNAEQAGQVFNVRDNEPLF 371
Db 178 LITRPALEKHLHLLDHPHVEILGFSEARKEYFYKYFHNAEQAGQVFNVRDNEPLF 237
QY 372 TMCVPLVWVCTCLOQQLGEGGLLQTSRTTAVYMLYLLSLMOPKPGAPRLQPPNQ 431
Db 238 TMCVPLVWVCTGLKQMESGKSLAQTSTTTAVYVFFLSLLQPRGGSQEHRLCAHL 297
QY 432 RGLCSLAADGLWNQKILFEEDLRKHGLDGEVSFAFLNMI FOKINCERYYSFIHLSFQ 491
Db 298 WGLCSLAADGIWNQKILFEESDLRNHGLQKADVSFAFLNMLFQKEDVCEKFIYFIHMTFQ 357
QY 492 EFFAAMYIILDEGGAG-----PDQDVTRLLTEYAFSERSFIALTSRFLGLNNE 542
Db 358 EFFAAMYILLEEKERRTNIPGSRLLKPSRDVTVLLENYKFKGYLIFVVRFLGLVNG 417
QY 543 ETRSHLEKSLCWKSPHIMDLLOWIQSKAQSDGSTLQOQSLEFPSCLYIEQEEFTQQA 602
Db 418 ERTSYLEKSLCKISQIRLELLKWEVAKAKKLIQPSQLELFYCLYEMQEEDFVQRA 477
QY 603 LSHFQVIVVSNIAKMEHVMVSSFCCLKRC 630
Db 478 MDYFPKIEI-NLSTRMDHVSVSFCIENC 504
RESULT 11
Q68U60 PRELIMINARY; PRT; 506 AA.
ID Q68U60
AC Q68U60;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Cryopyrin (Fragment).
GN Name=CIAS1;
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302403; DOI=10.1016/j.gene.2004.05.002;
RA Anderson J.P., Mueller J.D., Rosengren S., Boyle D.L., Schaner P.,
RA Cannon S.B., Goodyear C.S., Hoffman H.M.;
RT "Structural, expression, and evolutionary analysis of mouse CIAS1.";
RL Gene 338:25-34(2004).
DR EMBL: AY338197; AAR03566.1; -.
SQ
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RT "Structural, expression, and evolutionary analysis of mouse CIAS1.";
RL Gene 338:25-34(2004).
DR EMBL: AY338198; AAR03567.1; -.
DR InterPro: IPR007111; NACHT_NTPase.
DR Pfam: PF05729; NACHT, 1.
DR PROSITE: PS50837; NACHT, 1.
FT NON_TER 1
FT NON_TER 506
FT SEQUENCE 506 AA; 58812 MW; F8AC1357A5087C5E CRC64;
SQ
Query Match 27.0%; Score 1475.5; DB 2; Length 506;
Best Local Similarity 54.7%; Pred. No. 1.6e-96;
Matches 278; Conservative 98; Mismatches 119; Indels 13; Gaps 4;
QY 132 RLLLVKHSNPMQVQQQLDTCGRHARTVGHQAQSPKIETLFFPDEERPEPPRTVMVQGA 191
Db 1 RRLVKEHRSQOEREHELLAIGK--TKTLESPVPIKWEMLFPDDHESEPHVTVVQGA 58
QY 192 AGIGKSMIAHKVMDWADGKLFQGRFDYLFYINCRMNQSAATSCSMQDLIFSCWPEPSAP 251
Db 59 AGIGKTLARKIMLDWASGTLYQDRFDYLFYIHCREVS-LVTQSLGDLIVSCCPDPNPP 117
QY 252 LOELIRVPERLLFIIDGDELKPSFHDQPGWCLWEEKRPTTELLNSLRKLLPELSL 311
Db 118 IRKIVSKPSRIILFMDGDFDELQAFDEHIGPLCTDWQKAERGDIILSSLRKLLPEASL 177
QY 312 LITRPTALEKHLRLLHPHVEILGFSEARKEYFYKYFHNAEQAGQVFNVRDNEPLF 371
Db 178 LITRPALEKHLHLLDHPHVEILGFSEARKEYFYKYFHNAEQAGQVFNVRDNEPLF 237
QY 372 TMCVPLVWVCTCLOQQLGEGGLLQTSRTTAVYMLYLLSLMOPKPGAPRLQPPNQ 431
Db 238 TMCVPLVWVCTGLKQMESGKSLAQTSTTTAVYVFFLSLLQPRGGSQEHRLCAHL 297
QY 432 RGLCSLAADGLWNQKILFEEDLRKHGLDGEVSFAFLNMI FOKINCERYYSFIHLSFQ 491
Db 298 WGLCSLAADGIWNQKILFEESDLRNHGLQKADVSFAFLNMLFQKEDVCEKFIYFIHMTFQ 357
QY 492 EFFAAMYIILDEGGAG-----PDQDVTRLLTEYAFSERSFIALTSRFLGLNNE 542
Db 358 EFFAAMYILLEEKERRTNIPGSRLLKPSRDVTVLLENYKFKGYLIFVVRFLGLVNG 417
QY 543 ETRSHLEKSLCWKSPHIMDLLOWIQSKAQSDGSTLQOQSLEFPSCLYIEQEEFTQQA 602
Db 418 ERTSYLEKSLCKISQIRLELLKWEVAKAKKLIQPSQLELFYCLYEMQEEDFVQRA 477
QY 603 LSHFQVIVVSNIAKMEHVMVSSFCCLKRC 630
Db 478 MDYFPKIEI-NLSTRMDHVSVSFCIENC 504
RESULT 11
Q68U60 PRELIMINARY; PRT; 506 AA.
ID Q68U60
AC Q68U60;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Cryopyrin (Fragment).
GN Name=CIAS1;
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15302403; DOI=10.1016/j.gene.2004.05.002;
RA Anderson J.P., Mueller J.D., Rosengren S., Boyle D.L., Schaner P.,
RA Cannon S.B., Goodyear C.S., Hoffman H.M.;
RT "Structural, expression, and evolutionary analysis of mouse CIAS1.";
RL Gene 338:25-34(2004).
DR EMBL: AY338197; AAR03566.1; -.
SQ
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DR InterPro; IPR007111; NACHT_NTPase.

DR Pfam; PF05729; NACHT; 1.

DR PROSITE; PS50837; NACHT; 1.

FT NON_TER 1

FT NON_TER 506

SQ SEQUENCE 506 AA; 58737 MW; 3355BE2362CD008 CRC64;

Query Match 27.0%; Score 1475.5; DB 2; Length 506;

Best Local Similarity 54.7%; Pred. No. 1.6e-96;

Matches 278; Conservative 98; Mismatches 119; Indels 13; Gaps 4;

Qy 132 RLLVKEHSNPMQVQQLDTRGHARTVGHQAASPIKETLFEPEDEERPEPRPTVMQGA 191

Db 1 RRLIKEHRSQEREHELLAIGK--TKTWSPVSPKIMELLFPDDHSEEPVHTVVFQGA 58

Qy 192 AGIGKSLAHKMLDWDADGKLFQGRFDYLFYINCRMNQSAATECSMODLIPSCWPEPSAP 251

Db 59 AGIGKTLARKIMLDWASGTYLQDRFDYLFYIHCREVS-LVTQSLGDLINSCCPDPNP 117

Qy 252 LQELIRVPERLFIIDGDELKPSFHDPPQGPWCWCWEKRPTELLINSLIRKLLPELSL 311

Db 118 IRKIVKPSRILFLMDGDFDELQGAFFDEHIGPLCTDWQKAERGDILLSSLRKLLPEASL 177

Qy 312 LITTRPALEKHLRLLHPRHVEILGFSEARKEYFYKYFHNAQAGOVFNVRDNEPLF 371

Db 178 LITTRPALEKHLRLLHPRHVEILGFSEARKEYFYKYFHNAQAGOVFNVRDNEPLF 371

Qy 372 TMCVPLVWVCTCLOQLEGGLLROTSTRTTAVMYLLSLMQPKPGAPRLQPPNQ 431

Db 238 TMCVPLVWVCTCLOQLEGGLLROTSTRTTAVMYLLSLMQPKPGAPRLQPPNQ 431

Qy 432 RGLCSLAADGLWNQKILFEEDLRKHGLDGEDVSAFLNMNIFOKDINCRYYSFIHLSFQ 491

Db 298 WGLCSLAADGLWNQKILFEEDLRKHGLDGEDVSAFLNMNIFOKDINCRYYSFIHLSFQ 491

Qy 492 EPPAAMYILDEGGGAG-----PDQDVTLLTEYAFSRSFLALTSRFLFGLNE 542

Db 358 EPPAAMYLLBEEKEGRTNPGSKLPSRDTVLLNENYKFKGYLIFVVRFLFGLVQ 417

Qy 543 ETRSHLEKSLCWKSPHIMKMDLLQWIOSKAQSGSTLQOQSLEFPSCLYEQIEEFIOQA 602

Db 418 ERTCYLEKLSCKISQIRLELLKWIIEVAKAKLQIQPSQLELYCYLMEQSDVFQRA 477

Qy 603 LSHFQIVVSNIAKMEHVVSSFCIKRC 630

Db 478 MDYFPKIEI-NLSTRMDHVVSSFCIENC 504

RESULT 12

Q68U56

ID Q68U56

AC Q68U56

DT 25-OCT-2004

DT 25-OCT-2004

DE Cryopyrin

GN Name=CIAS1;

OS Alouatta

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;

OC Alouatta

OX NCBI_TaxID=30590;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15302403; DOI=10.1016/j.gene.2004.05.002;

RA Anderson J.P., Mueller J.L., Rosengren S., Boyle D.L., Schaner P.,

RA Cannon S.B., Goodyear C.S., Hoffman H.M.;

RA "Structural, expression, and evolutionary analysis of mouse CIAS1";

RL Gene 338:25-34(2004).

DR EMBL; AY338201; AAR03570.1; -

DR InterPro; IPR007111; NACHT_NTPase.

DR Pfam; PF05729; NACHT; 1.

DR PROSITE; PS50837; NACHT; 1.

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FT NON_TER 500

SQ SEQUENCE 500 AA; 57619 MW; 0761E81FEE4ED92 CRC64;

Query Match 26.9%; Score 1474; DB 2; Length 500;

Best Local Similarity 56.1%; Pred. No. 2e-96;

Matches 282; Conservative 89; Mismatches 118; Indels 14; Gaps 5;

Qy 133 LLLVKEHSNPMQVQQLDTRGHARTVGHQAASPIKETLFEPEDEERPEPRPTVMQGA 192

Db 2 LRLIKEHRSQEREHELLTIGR--TKTADSPVSPKIMELLFPDAEHSEPHVHTVVFQGA 59

Qy 193 GIGKSLAHKMLDWDADGKLFQGRFDYLFYINCRMNQSAATECSMODLIPSCWPEPSAPL 252

Db 60 GIGKTLARKIMLDWASGTYLQDRFDYLFYIHCRELS-LVTQSLGDLINSCCPDPNPI 118

Qy 253 QELIRVPERLFIIDGDELKPSFHDPPQGPWCWCWEKRPTELLINSLIRKLLPELSL 312

Db 119 HKIVKPSRILFLMDGDFDELQGAFFDEHIGPLCTDWQKAERGDILLSSLRKLLPEASL 178

Qy 313 IITRPTALEKHLRLLHPRHVEILGFSEARKEYFYKYFHNAQAGOVFNVRDNEPLF 372

Db 179 VITRPALEKHLRLLHPRHVEILGFSEARKEYFYKYFHNAQAGOVFNVRDNEPLF 372

Qy 373 MCFVPLVWVCTCLOQLEGGLLROTSTRTTAVMYLLSLMQPKPGAPRLQPPNQ 432

Db 239 MCFVPLVWVCTCLOQLEGGLLROTSTRTTAVMYLLSLMQPKPGAPRLQPPNQ 432

Qy 433 GLCSLAADGLWNQKILFEEDLRKHGLDGEDVSAFLNMNIFOKDINCRYYSFIHLSFQ 492

Db 299 GLCSLAADGLWNQKILFEEDLRKHGLDGEDVSAFLNMNIFOKDINCRYYSFIHLSFQ 492

Qy 493 EPPAAMYILDEGGGAG-----PDQDVTLLTEYAFSRSFLALTSRFLFGLNE 542

Db 359 EPPAAMYLLBEEKEGRTNPGSKLPSRDTVLLNENYKFKGYLIFVVRFLFGLVQ 418

Qy 543 ETRSHLEKSLCWKSPHIMKMDLLQWIOSKAQSGSTLQOQSLEFPSCLYEQIEEFIOQA 602

Db 419 ERTSYLEKLSCKVSKSQIRLELLKWIIEVAKAKLQIQPSQLELYCYLMEQSDVFQSA 478

Qy 603 LSHFQIVVSNIAKMEHVVSS 625

Db 479 MDYFPKIEI-NLSTRMDHVVSS 500

RESULT 13

Q68U53

ID Q68U53

AC Q68U53

DT 25-OCT-2004

DT 25-OCT-2004

DE Cryopyrin

GN Name=CIAS1;

OS Cebus apella

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.

OC NCBI_TaxID=9515;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15302403; DOI=10.1016/j.gene.2004.05.002;

RA Anderson J.P., Mueller J.L., Rosengren S., Boyle D.L., Schaner P.,

RA Cannon S.B., Goodyear C.S., Hoffman H.M.;

RA "Structural, expression, and evolutionary analysis of mouse CIAS1";

RL Gene 338:25-34(2004).

DR EMBL; AY338204; AAR03573.1; -

DR InterPro; IPR007111; NACHT_NTPase.

DR Pfam; PF05729; NACHT; 1.

DR PROSITE; PS50837; NACHT; 1.

FT NON_TER 1

FT NON_TER 500

SQ SEQUENCE 500 AA; 57708 MW; 055D921C39DDB6D7 CRC64;

Query Match	26.9%;	Score 1471;	DB 2;	Length 500;
Best Local Similarity	55.9%;	Pred. No. 3.3e-96;		
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			Indels	14;
			Gaps	
133	LLLVKHSNPMVQOQLLDTGRGHARTVGHQASPIKIEIPLFEDEPERPEPRTVMVQAA	192		
2	LRLKEHRSQERQELLTGR--TKTGDSVPSPIKMELLFEPDAHSEPHVTVVFGAA	59		
193	GIGKSMIAHVMILMDWADGKLFGQRPDYLFVINCENMQSATSCSQMDLIFSCWPPSPAPL	252		
60	GIGKTI LARKIMLDWASGTLYQDRFDYLFYIHCRELS-LVTQRLSGDLIMSCCPDPNPPI	118		
253	QELIRVPERLFIIDGFEDELKPSFHPDQGPWCLCWEKEKPTPELLNSLRKLLKLLPELSLL	312		
119	HKIVRKPSRIFLMDGFEDELQAGDEHIGPLCTNWQAKERGDI LUSLLRKLKLLPEASLL	178		
313	ITTRPTALEKLRLLHPRHVEIILGFESEAKREKFYKYFHNAEQAGQVENVYVRDNEPLFT	372		
179	ITTRPVALEKQLHLDHPRHVEIILGFESEAKREKFYKYFSDEAQPRAAASLLQENEVLFT	238		
373	MCFPVLVCWVVCTCLOOQLGGGLLRQTSRTTTTAVMYLLLSLMQPKGAPRLQPPPNOR	432		
239	MCFTPLVCWIVCTGLKQOMESGKSLAQTSKTTTAVYIFLSSLLQPRGSGHPHLSAHLM	298		
433	GLCSLAADGLMNKILFEBODLRKHGLGDVEDSAFLNMNI FQDINCERYVYGFHLSFOE	492		
299	GLCSLAADGIMNQKILFEESDLRNHGKQADVSASFRLMNL FQKVEDCEKXFYFIHMTPOE	358		
493	FFAAMYIITLDSGEGGAG-----PDQDVTRLLTEYAFSRSFLATSLTSPFLGLLNE	542		
359	FFAAMYIYLLBENGGRTNVUGSCLITLPSRDVTVLLENYCKPEKGYLI FVWRFGLGVNQ	418		
543	ETRSHLEKSLCWKVSPIHKMDLLQWIOKSAQSDGSTLQQSGSLFFPFCLEI QEEETFOA	602		
419	ERTSVLEKKLSCKVYSQQIRLELLAKWIEVAKAKKLIQPSQLELFCYLEMQEEAFVQRA	478		
603	LSHFQVIVVSNIAKQEHMVWSSP	625		
479	MDYFPFRIE-NLSTRMDHWVSSP	500		

RESULT	14
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AC	Q68U57;
DT	25-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Cryopyrin (Fragment).
GN	Name=CIASI;
OS	Colobus guereza (Black-and-white colobus monkey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC	Colobus.
OX	NCBI_TaxID=33548;
RN	[1]_TaxID=33548;
RP	SEQUENCE FROM N.A.
RX	PubMed=15302403; DOI=10.1016/j.gene.2004.05.002;
RA	Anderson J.P., Mueller J.L., Rosenberg S., Boyle D.L., Schaner P.,
RA	Cannon S.B., Goodyear C.S., Hoffman H.M.;
RL	"Structural, expression, and evolutionary analysis of mouse CIAS1."
RT	Gene 318:25-34(2004).
DR	EMBL; AY338200; AAR03569.1; ..
DR	InterPro; IPR007111; NACHT_NTPase.
DR	Fram; PF05729; NACHT; 1.
DR	PROSITE; PSS0837; NACHT; 1.
FT	NON TER
FT	1
FT	NON TER
FT	506
SO	SEQUENCE 506 AA; 58700 MW; 435425BC125BBAD4 CRC64;

Query Match	26.9%	Score 1470.5;	DB 2;	Length 506;
Best Local Similarity	54.5%	-Pred. No. 3.7e-96;		
Matches 277; Conservative	98;	Mismatches 120;	Indels 13;	Gaps 4;

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132 RLLLVKEHSNPMQVOOQLDLOGRHARTVGHQAQSPKIEIETLPEDEPERPPRVVMQGA 191
1 RURLIKEHRSQOEREHEHLLAICK--TKTCESFVSPKIMELLFPDDBSHEVHTVTFQGA 58
192 AGIGSMIAHKYMLDOWADGKLFQGRFDYLFVINCREMNOQATEGSMODLIPSCWPPEPAP 251
59 AGIGKTLILARKIMDOWAGSTLYRDFDYLFIYHCREVS-LVTQSLGDLIMSCCPDENPP 117
252 LOELIRVPERLLFIIDGDELUKPSPHDPOGPGWCLCWEKRPTELLINSLIRKLLPELSL 311
118 IRKIVSKPSKILFLMDGDELOQAFDEHIGLCTDQKAERGDILLSLIRKLLPEASL 177
312 LITTRTALFKLHRLHPRHVEIILGFSEAEKKEYFYKYPHNAEQAGOVFVNYVRDNEPLF 371
178 LITTRVVALEKLOHLLDHPRHVEIILGFSEAKKEYFFKYFSDAQARAASFSLIQENEVL 237
372 TMCFVPLVCVWVCTCLOQOEGGLLROTSPRTTAYMYLLSLMQPKPGAPRIQPPNQ 431
238 TMCFIPLCVWVCTGLKQOMSEKSLAOTSKTTTAVYTFISLLQPRGSGHEHLCAHL 297
432 RGLCSLAADGLANOKILPEEQDLRKHGLDGEDVSAFLNMNIFOKDINCERYVSFIHLSEFQ 491
298 WGLCSLAADGIWNQKILFEESDLRNHGLQADVSFLRNNLFOKEVDCEKYSFIHMTFQ 357
492 EFFAAMYIILDEGEGGAG-----PDQVTRLITLYAFSERSERFIALTSRFLGLELINE 542
358 EFFAAMYILLEEBEGKRTNVPGSRLKLPDRDVTVLLENYKGFEKGYLLFVVRFLFGLVNO 417
543 ETASHILEKSLCWKVSPHIKMDLLOWTOSKAQSDGSTLOQGSLEFFYSCLYEIQEEEFIOQA 602
418 ERTCYLEKSLCKISQOIRLELLUKLWIEVAKAKWQIQPSQLELYFCLYEMQEEDFVQRA 477
603 LSHFQVITVWSNIASKMEHVMVSFCLKRC 630
478 MYPEKPIET--NLSTRMDHVVYSSFCIENC 504

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RESULT 15
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AC Q68U58;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Cryopyrin (Fragment).
GN Name:CIAS1;
OS Cercopithecus cephus (moustached monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9535;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed:15302403; DOI=10.1016/j.gene.2004.05.002;
RA Anderson J.P., Mueller J.S., Rosengren S., Boyle D.L., Schaner P.,
RA Cannon S.B., Goodyear C.S., Hoffman H.W.;
RT "Structural, expression, and evolutionary analysis of mouse CIAS1.";
RL Gene 338:25-34(2004).
DR EMBL; AY338199; AAR03568.1; -.
DR InterPro; IPR007111; NACHT_NTPase.
DR Pfam; PF05729; NACHT; 1.
DR PROSITE; PS50837; NACHT; 1.
FT NON TER 1
FT NON TER 506
FT NON TER 506
SO SEQUENCE 506 AA; 58807 MW; 3BD8387BC8ACBB63 CRC64;

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Query Match      26.8%; Score 1468.5; DB 2; Length 506;
Best Local Similarity 54.5%; Pred.No. 5.1e-96;
Matches 277; Conservative 98; Mismatches 120; Indels 13; Gaps 4;

QY 132 RLLLVKHSNPVQVOQLDTCRGHARTVGHQASPIKIETLFEDESRPPPTVVMOGA 191
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2005, 14:41:25 ; Search time 46 Seconds
(without alignments)
1679.604 Million cell updates/sec

Title: US-10-781-294-24
Perfect score: 5472
Sequence: 1 MLRTAGDGLCRSLSTYLEEL.....MTHSRLAALRVTKPYLDIGC 1035

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1375	25.1	1454	4	US-09-388-221B-10
2	1375	25.1	1473	4	US-09-388-221B-2
3	1360	24.9	1399	4	US-09-388-221B-4
4	1360	24.9	1424	4	US-09-388-221B-12
5	1360	24.9	1443	4	US-09-388-221B-6
6	723	13.2	461	2	US-08-910-731-6
7	717	13.1	456	2	US-08-910-731-4
8	717	13.1	456	2	US-08-795-395-4
9	712	13.0	456	2	US-08-910-731-8
10	709	13.0	456	2	US-08-910-731-2
11	709	13.0	456	2	US-08-795-395-2
12	529	9.7	1013	4	US-10-014-269-3
13	529	9.7	1040	4	US-10-014-269-2
14	529	9.7	1043	4	US-09-949-016-9080
15	526	9.6	1040	4	US-10-014-269-4
16	522	9.5	953	3	US-09-099-041A-8
17	522	9.5	953	3	US-09-245-281-8
18	522	9.5	953	4	US-09-207-359B-8
19	522	9.5	953	4	US-09-340-620A-8
20	522	9.5	953	4	US-09-865-364-8
21	511	9.3	1007	4	US-10-014-269-34
22	498.5	9.1	209	4	US-09-388-221B-19
23	464.5	8.5	953	3	US-09-245-281-43
24	464.5	8.5	953	4	US-09-207-359B-43
25	464.5	8.5	953	4	US-09-340-620A-43
26	464.5	8.5	953	4	US-09-865-364-43
27	455.5	8.3	966	4	US-09-207-359B-47

28	455.5	8.3	966	4	US-09-865-364-47	Sequence 47, Appl
29	377.5	6.9	830	4	US-09-064-199-19	Sequence 19, Appl
30	377.5	6.9	1106	4	US-09-064-199-17	Sequence 17, Appl
31	377.5	6.9	1130	2	US-08-519-547A-6	Sequence 6, Appl
32	377.5	6.9	1130	4	US-09-064-199-18	Sequence 18, Appl
33	377.5	6.9	1207	4	US-09-064-199-16	Sequence 16, Appl
34	315	5.8	490	3	US-09-099-041A-26	Sequence 26, Appl
35	315	5.8	490	3	US-09-245-281-26	Sequence 26, Appl
36	315	5.8	490	4	US-09-207-359B-26	Sequence 26, Appl
37	315	5.8	490	4	US-09-340-620A-26	Sequence 26, Appl
38	315	5.8	490	4	US-09-865-364-26	Sequence 26, Appl
39	301.5	5.5	320	4	US-10-014-269-30	Sequence 30, Appl
40	287.5	5.3	305	4	US-10-014-269-7	Sequence 7, Appl
41	261	4.8	212	4	US-09-388-221B-20	Sequence 20, Appl
42	245	4.5	200	3	US-09-099-041A-11	Sequence 11, Appl
43	245	4.5	200	3	US-09-245-281-11	Sequence 11, Appl
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45	245	4.5	200	4	US-09-340-620A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-388-221B-10
; Sequence 10, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Construct
US-09-388-221B-10

Query Match	25.1%	Score 1375;	DB 4;	Length 1454;
Best Local Similarity	33.9%	Pred. No. 9.2e-126;		
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Db	8	RLACYLEFLKKEELKEFQLLLANKAHSSSSGETP-AQPEKTSQMEVASYLVAQYGEQRA	66	
Qy	70	WRLALSTFERINRKDLWEGOR-----EDLVRDPQETRYDYV-----	106	
Db	67	WDLALHTWEGMGRSLCAQAEQAGHSPSPSPSEPHLGSPSOFTSTAVLMPWIHELPA	126	
Qy	107	-----RRKFRMEDRNALGECVNLSHRYTRILLVKEHNSPMQVQ-----	146	
Db	127	GCTOGSERRVLRLPDTISGRWRWEISASLLYQALPSSPDHESPSQESNAPTSTAVLGSW	186	
Qy	147	-----	146	
Db	187	GSPQPSLAPREQEAPGTQWPLDTSIGYVTEIREREREREKSEKGRPPWAAVVGTPPOAHT	246	
Qy	147	-----	160	
Db	247	SLOPHHHWPSVRESLCSTWPKNEDFNOKFTOLLQLLQRPHPRSQDPLVKRSPDYVEE	306	
Qy	161	--GHQASPIKIEITLFEPEDEERPEPRPTVMQGAAGIKGSMIAHVKMLMDWADKLFQGRFD	218	
Db	307	NRGHL---IEIRDLFGGLTQEQ-PRVILQGAAGIKSTLARQVKANGRGQLYGDQFQ	362	
Qy	219	YLFYINCREMNQSCATECSMODLIFSCWPEPSAPIQLIRVPERLLFIIDGDELKPSFHD	278	

Db 363 HVFYFSCRELAQSKV-VSLAELIGKDGATAPAPIRQILSRPERLLFILGDVDEPGWVLQ 421
Qy 279 PQGPWCLCWEKRPTELLNSLRKXKLLPELSLLITRPTALEKHLRLEHPRHVEILGF 338
Db 422 PSELCHWSPQPADALLGSLGKTLPEASPLITARTALQNLIPSLQEARWVEVLGF 481
Qy 339 SEAEKEYFYKYPHNAEQOVNRYDRNEPLFTMCFVPLVCWVCTCLQQOEGGGLLR 398
Db 482 SESSKEYFYRYTDERQAIRAFRLVKSNEKELWALCLVPWVSLACTCLMQQKREKLT 541
Qy 399 QTSRTTAVVMLYLLSMQPKAPRLQPPNQRGLCSLAADGLMNQKILFEEQDLRKHG 458
Db 542 LTKTITTLCHYLAQALQPLGQPL-----RDLCSLAAGIWKQKTLFSPDDLRKHG 595
Qy 459 LDGEDVSFAFNMIQKIDNCERYYSFIHLSPOEFPAAMYIILDEGEGAGPDQ----DV 514
Db 596 LDGAISTFLKMGILQEH-PIPLSYSFHLCFOEFPAAMSYVL-EDEKGRGKHSNCIIDL 653
Qy 515 TRLLTEYAFSERSFLATSRFLGLNNEETRSHEKSLCWKVSPIHKMDLLOWIQSKAQS 574
Db 654 EKTLEYAGI-HGLFGASTTRFLGLLSDEGEREMENIFHCRLSQ--GRNLMQWVPSLQ-- 708
Qy 575 DGSTLQOGLSLEFFSCLYEIOEBEFTQOALSHFQVIVVSNIAKQVHMVSSFCCLKRCRSAQ 634
Db 709 --LLQPHSLSLHCLYETRNKTLFTQVMAHFPEMGMC-VETDMELLVCTFCIKFSRHVK 765
Qy 635 VHLHYGATYADGEDRARCAGATLLVQLRPERVLLDAYSEHLAAALCTNPNLIELSL 694
Db 766 KLQLI-----EGRQHRSTWSPWVLF--WVPVTDAYWQLFSLVKVTRNLKELD 815
Qy 695 YRNALSGRVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSGN 754
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Qy 755 GVGFPGMMLCEGLRHPQCRLOMTQLRKQLESACQEMASVLGTNPHILVELDLTGNALE 814
Db 876 VLTDAAGAKHLQRLRQPSCKLQRLQVSCGLTSDCCQDLASVLSASPSLKELDLQNNLD 935
Qy 815 DLGRLILCOGLRHPVCRILRLTWLKI CRLTAAACDELASTLSVNQSLRELDLSNEL---- 870
Db 936 DVGVRLLCEGLRHPACKLIRLGL-----DQTLSDMEQELRALEQEPQLLIFS 985

RESULT 2

US-09-388-221B-2
; Sequence 2, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-388-221B-2
Query Match 25.1%; Score 1375; DB 4; Length 1473;
Best Local Similarity 33.9%; Pred. No. 9.4e-126;
Matches 366; Conservative 138; Mismatches 357; Indels 218; Gaps 23;
Qy 12 RLSTYLEEAEVLEKFKLYLCTA--TELGEKIPWGSMEKAGPLEMAQLLITHFGPEEA 69
Db 8 RLACYLEFLKKELEFQLLLANKAHSRSSGETP-AQPEKTSNGNEVASYLVAQYGEORA 66

Qy 70 WRLALSTPERINRKDLMERGOR-----EDLVDPQPTYRDYV----- 106
Db 67 WDLALHTWEQWGLSLSLCAQAQEGAGHSPSPYPSPSEPHLGSQPTSTAVLMPWIHELPA 126
Qy 107 -----RRKPRMEDNRNARLGEVCUNLSHRYTRLLLVKEHSNPMQVQ----- 146
Db 127 GCTGSGERRVLROLPDTSGREWRREISASLLYQALFSSPDHESPSQESNAPTSTAVLGSW 186
Qy 147 ----- 146
Db 187 GSPPOPSLAPREQEAPGTQWPLDETSGIYITEIREREREKSEKGRPPWAAVVGTPPQAHT 246
Qy 147 -----QQLDTRGRHARTV----- 160
Db 247 SLQPHHHWPSPVRESLCTWPKNEDFNQKFTQLLLQRPHPRSQDPLVKRSPDYVEE 306
Qy 161 --GHOASIKIETLPEPDEERPEPRVTVMOGAGIGKSLAHKMLMDWADGKLFQGRFD 218
Db 307 NRGHU---TEIRDLPFGPLDQOE-PRVILQOAGIGKSTLARQVKEAGRGQLYGDPRQ 362
Qy 219 YLFYINCREMNOQATECSMDLIFSCWPEPSAPLQELIRVPERLLFIIDGDELKPSPHD 278
Db 363 HVFYFSCRELAQSKV-VSLAELIGKDGATAPAPIRQILSRPERLLFILGDVDEPGWVLQ 421
Qy 279 PQGPWCLCWEKRPTELLNSLRKXKLLPELSLLITRPTALEKHLRLEHPRHVEILGF 338
Db 422 PSELCHWSPQPADALLGSLGKTLPEASPLITARTALQNLIPSLQEARWVEVLGF 481
Qy 339 SEAEKEYFYKYPHNAEQOVNRYDRNEPLFTMCFVPLVCWVCTCLQQOEGGGLLR 398
Db 482 SESSKEYFYRYTDERQAIRAFRLVKSNEKELWALCLVPWVSLACTCLMQQKREKLT 541
Qy 399 QTSRTTAVVMLYLLSMQPKAPRLQPPNQRGLCSLAADGLMNQKILFEEQDLRKHG 458
Db 542 LTKTITTLCHYLAQALQPLGQPL-----RDLCSLAAGIWKQKTLFSPDDLRKHG 595
Qy 459 LDGEDVSFAFNMIQKIDNCERYYSFIHLSPOEFPAAMYIILDEGEGAGPDQ----DV 514
Db 596 LDGAISTFLKMGILQEH-PIPLSYSFHLCFOEFPAAMSYVL-EDEKGRGKHSNCIIDL 653
Qy 515 TRLLTEYAFSERSFLATSRFLGLNNEETRSHEKSLCWKVSPIHKMDLLOWIQSKAQS 574
Db 654 EKTLEYAGI-HGLFGASTTRFLGLLSDEGEREMENIFHCRLSQ--GRNLMQWVPSLQ-- 708
Qy 575 DGSTLQOGLSLEFFSCLYEIOEBEFTQOALSHFQVIVVSNIAKQVHMVSSFCCLKRCRSAQ 634
Db 709 --LLQPHSLSLHCLYETRNKTLFTQVMAHFPEMGMC-VETDMELLVCTFCIKFSRHVK 765
Qy 635 VHLHYGATYADGEDRARCAGATLLVQLRPERVLLDAYSEHLAAALCTNPNLIELSL 694
Db 766 KLQLI-----EGRQHRSTWSPWVLF--WVPVTDAYWQLFSLVKVTRNLKELD 815
Qy 695 YRNALSGRVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSGN 754
Db 816 SGNLSHSAVKSCKTLRPRCLLETURLAGCGLTAECDCKDLAFGLRANQTLTDLDFN 875
Qy 755 GVGFPGMMLCEGLRHPQCRLOMTQLRKQLESACQEMASVLGTNPHILVELDLTGNALE 814
Db 876 VLTDAAGAKHLQRLRQPSCKLQRLQVSCGLTSDCCQDLASVLSASPSLKELDLQNNLD 935
Qy 815 DLGRLILCOGLRHPVCRILRLTWLKI CRLTAAACDELASTLSVNQSLRELDLSNEL---- 870
Db 936 DVGVRLLCEGLRHPACKLIRLGL-----DQTLSDMEQELRALEQEPQLLIFS 985
Qy 871 -GDGLVLLCEGL-----RHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNLRELDLS 923
Db 986 RRKPSVMTPEGLDTGEMSNSTSLKQRLGSRASASHV-----AQANLKLDDVS 1035

RESULT 3

US-09-388-221B-4
; Sequence 4, Application US/09388221B
; Patent No. 6818750

QY	339	SEARKEYFYKYFHNAEQAGOVFNVDNEPLFTMCVFPLVCVWVCTCLOQLEGGLLR	398
Db	482	SSSRKEYFYRYFTDERQAIRAFRLVKSNEKELWALCLVFWVSWLACTCLCMQMKRKEKLT	541
QY	399	QTSRTTAVVYMLLSMQPKGAPRLQPPNORGLCSLAADGLWNOKILFEEQDLRKHG	458
Db	542	LTSKTTITLCHYLAAQALQPLGPOL-----RDLCSLAAEGIWQKTLFSPDDLKHG	595
QY	459	LDGEDVSAFLNMIFOKINCERYYSFIHLSFOEFFAAMYIILDEGEGGAGPDQ----	514
Db	596	LDGAILSTFLKMGILQEH-PIPLSYSFILHLCFOEFFAAMSYVL-EDEKGRGKHNCCIIDL	653
QY	515	TRLITEYAFSERSFALTSRFLGCLLNEETRSKLSKWCVPKSPHIMDOLLQWISKAQS	574
Db	654	EKTLVAYGI-HGLFGASTTRFLGLLSDEGEREMENIFHCRLSQ--GRNLQWVPSLQ--	708
QY	575	DGSTLOQGSLEFFSCLYIEEBEPIQALSHFQVIVVSNIAKWEHVVSSFCIKRCSAQ	634
Db	709	--LILQPHSLESILHCLYETRNKTLFTQVMAHFEEMGMC-VETDMELLVCTFCIKFSRHVK	765
QY	635	VLHLYGATYSADGEDRARCAGAHLLVQLRPRTVLLDAYSEHLAAALCTNPNLIELSL	694
Db	766	KLQILI-----EGRQHRSTWSPMTVFLR--WVPVTDAYWQILFSLVKVTRNLKELDL	815
QY	695	YRNALSGRGVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSGN	754
Db	816	SGNSLSHSAVKSCKTLRPRCLLETFLRAGCGLTAEDCKDLAFGLRANQTLTELDLSFN	875
QY	755	GVGFPGMMLCEGLRHPQCRLOMIQLRKQLESAGCOEMASVLGTPHVELDLTGNALE	814
Db	876	VLTDAGAKHLQRLQPSCKLQRLQVSCGLTSDDCQDLASVLSASPSLKELDLQNNLD	935
QY	815	DLGLRLCOGLRHPVCRILTLMWKICRLTAACDELASTLSVNSQSLRELDLSINELGDIG	874
Db	936	DVGVELLCEGLRHPACK-----LIRLGKPS	960
QY	875	VLLICEGL-----RHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNLRELDLS	923
Db	961	VMTPTTEGLDTGEMSNSTSSLRQRLGSEAAASHV-----AQANLKLLDVS	1005
RESULT 5			
US-09-388-221B-6			
; Sequence 6, Application US/09388221B			
; Patent No. 6818750			
; GENERAL INFORMATION:			
; APPLICANT: Reed, John C.			
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation			
; FILE REFERENCE: P-LJ 3650			
; CURRENT APPLICATION NUMBER: US/09/388,221B			
; CURRENT FILING DATE: 1999-09-01			
; NUMBER OF SEQ ID NOS: 30			
; SOFTWARE: Patent In Ver. 2.0			
; SEQ ID NO 6			
; LENGTH: 1443			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-388-221B-6			
Query Match 24.9%; Score 1360; DB 4; Length 1443;			
Best Local Similarity 33.5%; Pred. No. 2.7e-124;			
Matches 360; Conservative 133; Mismatches 343; Indels 238; Gaps 22;			
QY	12	RLSTYILEEAVELKFKLYLGTAA--TELGEKIPWGSMEKAGPLEMAQLLTHFGPEEA	69
Db	8	RLACYLEFLKKEELKEFQLLANKAHSRSSGETP-AQPEKTSGEVASYLVAQYGEQRA	66
QY	70	WRLLASTFERINKDLWERGQR-----EDLVDPQETRYDYV	106
Db	67	WDLALHTWEQMLRSLCAQAGAGHSPGFPYSPBFLGSPSQPTSTAVLPMWIHELPA	126
QY	107	-----RRKFLMEDNARLGCVNLSHRYFTLLLVKEHSNPMQVQ-----	146
RESULT 6			
US-08-910-731-6			
; Sequence 6, Application US/08910731			
; Patent No. 5932440			
; GENERAL INFORMATION:			
; APPLICANT: CHATTERJEE, DEB K.			
; APPLICANT: SHANDILYA, HARINI			
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof			
; NUMBER OF SEQUENCES: 16			
Db	127	GCTGGSERRVLRQLPDTSGRRWREISASLLYQALPSSPDHESPSQSPNAPTSTAVLGSW	186
QY	147	-----	146
Db	187	GSPQPSLAPREQAPCTOWPLDETSGIYYTEIREREREKSEKGRPPWAAVGTTPQAH	246
QY	147	-----QQLDTRGHARTV-----	160
Db	247	SLQPHHPWPSVRESLCSSTWPKNEDFNQFTQLLLQRPSPSQDPLVKRSPWDYVEE	306
QY	161	--GHOASPIKIEITLFEDEERPEPPRVVMQAGAGICKMLAHKMLMDWADGKLFQGRFD	218
Db	307	NRGHL---IEIRDLFGPLDTQE--PRIVILQGAAGICKSTARQVKEAWRGOLYGRFQ	362
QY	219	YLFVINCENMOSATESMODLIFSCWPSPSAPLOELIRVPERLLFIIDGFDLKPSPHD	278
Db	363	HVFYFSCRLAQSKV-VSLAELIKDGTATPAPRIQLSRPERLLFLDGVDEPGWVLOE	421
QY	279	POGWCMLCWEKRPTEILNLSLIRKLLPELSLITTRPTALEKHLRLEHPRHVEILGF	338
Db	422	PSSELCLHWSQPQADALLGSLGKLTILPEASFLITARTTALQNLIPSLQEARWVEVLG	481
QY	339	SEARKEYFYKYFHNAEQAGOVFNVDNEPLFTMCVFPLVCVWVCTCLOQLEGGLLR	398
Db	482	SSSRKEYFYRYFTDERQAIRAFRLVKSNEKELWALCLVFWVSWLACTCLCMQMKRKEKLT	541
QY	399	QTSRTTAVVYMLLSMQPKGAPRLQPPNORGLCSLAADGLWNOKILFEEQDLRKHG	458
Db	542	LTSKTTITLCHYLAAQALQPLGPOL-----RDLCSLAAEGIWQKTLFSPDDLKHG	595
QY	459	LDGEDVSAFLNMIFOKINCERYYSFIHLSFOEFFAAMYIILDEGEGGAGPDQ----	514
Db	596	LDGAILSTFLKMGILQEH-PIPLSYSFILHLCFOEFFAAMSYVL-EDEKGRGKHNCCIIDL	653
QY	515	TRLITEYAFSERSFALTSRFLGCLLNEETRSKLSKWCVPKSPHIMDOLLQWISKAQS	574
Db	654	EKTLVAYGI-HGLFGASTTRFLGLLSDEGEREMENIFHCRLSQ--GRNLQWVPSLQ--	708
QY	575	DGSTLOQGSLEFFSCLYIEEBEPIQALSHFQVIVVSNIAKWEHVVSSFCIKRCSAQ	634
Db	709	--LILQPHSLESILHCLYETRNKTLFTQVMAHFEEMGMC-VETDMELLVCTFCIKFSRHVK	765
QY	635	VLHLYGATYSADGEDRARCAGAHLLVQLRPRTVLLDAYSEHLAAALCTNPNLIELSL	694
Db	766	KLQILI-----EGRQHRSTWSPMTVFLR--WVPVTDAYWQILFSLVKVTRNLKELDL	815
QY	695	YRNALSGRGVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSGN	754
Db	816	SGNSLSHSAVKSCKTLRPRCLLETFLRAGCGLTAEDCKDLAFGLRANQTLTELDLSFN	875
QY	755	GVGFPGMMLCEGLRHPQCRLOMIQLRKQLESAGCOEMASVLGTPHVELDLTGNALE	814
Db	876	VLTDAGAKHLQRLQPSCKLQRLQVSCGLTSDDCQDLASVLSASPSLKELDLQNNLD	935
QY	815	DLGLRLCOGLRHPVCRILTLMWKICRLTAACDELASTLSVNSQSLRELDLSINELGDIG	874
Db	936	DVGVELLCEGLRHPACK-----LIRLGKPS	960
QY	875	VLLICEGL-----RHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNLRELDLS	923
Db	961	VMTPTTEGLDTGEMSNSTSSLRQRLGSEAAASHV-----AQANLKLLDVS	1005

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/910,731
;; FILING DATE: (Herewith)
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/795,395
;; FILING DATE: 04-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/794,546
;; FILING DATE: 03-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/024,057
;; FILING DATE: 16-AUG-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ESMOND, ROBERT W.
;; REGISTRATION NUMBER: 32,893
;; REFERENCE/DOCKET NUMBER: 0942.3440003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 461 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-910-731-6

Query Match 13.2%; Score 723; DB 2; Length 461;
Best Local Similarity 42.5%; Pred. No. 3.2e-62;
Matches 150; Conservative 64; Mismatches 139; Indels 0; Gaps 0;
Qy 671 LLDAYSEHLAAALCTNPNIJELSYRNALGSRGVKLLCOGLRHPNCKLQNLRLKRCRIS 730
Db 40 LTEARCKDIISALRVNPAELNRSNELGVDGVHCVLQGLQTSCKIQKLSLQNCCLTG 99
Qy 731 SACEDLSAALIANKNLTRMDLSGNGVPGPMMLCEGLRHPQCRQLQMIQLRKQLESGAC 790
Db 100 AGCGVLSSTLRTPTLQELHLSNLDGAGLQLLCEGLDPPQCRLEKQLEYCNSLSAASC 159
Qy 791 QEMASVLGTNPVHVELDLTGNALEDGLRLCCOGLRHPVCLRTLWIKICBLTAACDEL 850
Db 160 EPLASVLRAPDFKELTVSNNDINEAGVRLCCOGLKDSPPQLEALKLESCGVTSNCRDL 219
Qy 851 ASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPTCKIQLTRIGICRLGSAACEGLSVV 910
Db 220 CGIVASVKSRLAELGSKNGKLDGVMALCPGLLPPSRRLRTLWEGCITAKGCGDLCRV 279
Qy 911 LQANHNLRELDLSFNDLGDWGLWLLAEGLQHPACRLQKMLDSCGLTAKACENLYFTLGI 970
Db 280 LRAKESLKELSLGNELGDEGARLLCETLLPQGLSGLWVKSFTAACCPHFSSVLAQ 339
Qy 971 NQTLTDLVLTNNALGDTGVRLCKRLSHPGCKLRLVLMFGMDLNKMTSHRLAA 1023
Db 340 NRFLLEQLISNRLNEDAGVRELCOGLQPGSGVRLVLMADCDVSDSSCSLAA 392

RESULT 7
US-08-910-731-4
; Sequence 4, Application US/08910731

;; Patent No. 5932440
;; GENERAL INFORMATION:
;; APPLICANT: CHATTERJEE, DEB K.
;; APPLICANT: SHANDILYA, HARINI
;; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/910,731
;; FILING DATE: (Herewith)
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/795,395
;; FILING DATE: 04-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/794,546
;; FILING DATE: 03-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/024,057
;; FILING DATE: 16-AUG-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ESMOND, ROBERT W.
;; REGISTRATION NUMBER: 32,893
;; REFERENCE/DOCKET NUMBER: 0942.3440003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 456 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-910-731-4

Query Match 13.1%; Score 717; DB 2; Length 456;
Best Local Similarity 41.5%; Pred. No. 1.2e-61;
Matches 147; Conservative 66; Mismatches 141; Indels 0; Gaps 0;
Qy 671 LLDAYSEHLAAALCTNPNIJELSYRNALGSRGVKLLCOGLRHPNCKLQNLRLKRCRIS 730
Db 35 LTVRCCKDIISALQANPALTELSLRTNELGDAGVLVQLQNTCKIQKLSLQNCSLTE 94
Qy 731 SACEDLSAALIANKNLTRMDLSGNGVPGPMMLCEGLRHPQCRQLQMIQLRKQLESGAC 790
Db 95 AGCGVLPDVLRSLSLRELHNDNPLDGEGLKLLCEGLRDPQCRLEKQLEYCNSLTATSC 154
Qy 791 QEMASVLGTNPVHVELDLTGNALEDGLRLCCOGLRHPVCLRTLWIKICBLTAACDEL 850
Db 155 EPLASVLRVPDFKELTVLSNNDINEAGIHTLCCOGLKDSACQLESKLENCGITSANCKDL 214
Qy 851 ASTLSVNQSLRELDLSNELGDLGVLLCEGLRHPTCKIQLTRIGICRLGSAACEGLSVV 910
Db 215 CDVVASVKSRLAELGSKNGKLDGVMALCGLLLPSCRLRTLWMDCDVTAEGCKDLCRV 274
Qy 911 LQANHNLRELDLSFNDLGDWGLWLLAEGLQHPACRLQKMLDSCGLTAKACENLYFTLGI 970
Db 275 LRAKESLKELSLGNELKDEGAQLCELSLLEPGQLESVWVTKTSLTAASCPHFCSVLT 334
Qy 971 NQTLTDLVLTNNALGDTGVRLCKRLSHPGCKLRLVLMFGMDLNKMTSHRLAA 1024
Db 335 NSSLFLQMSNPLGDSGVVELCKALGYPTVRLVLMADCDVTDGSSSLATV 388

RESULT 8

US-08-795-395-4
; Sequence 4, Application US/08795395
; Patent No. 5965399
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Cloning and Expression of Rat Liver and
; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,395
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-395-4

Query Match 13.1%; Score 717; DB 2; Length 456;
Best Local Similarity 41.5%; Pred. No. 1.2e-61;
Matches 147; Conservative 66; Mismatches 141; Indels 0; Gaps 0;
QY 671 LLDAYSEHLAAALCTNPNIETSLYRNALSGRGVKKLCOGLRHPNCKLQNLKRCRIS 730
Db 35 LTVCKDIRSAIQANPALTELSRTNELGAGVGLVQLGQNTCKIQKLSQNCSLTE 94
QY 731 SACEDELSAALIANKNLTMRDLSGNGVFPFGMMLLCEGLRHPNCKLQNLKRCRIS 790
Db 95 AGCGVLPVLSRLSTLRHLNDPLGDEGLKLLCEGLRDPQCRLEKLEFCNLTATSC 154
QY 791 QEMASVLGTNPVHVELDTGNALDELGLRLCCOGLRHPNCKLQNLKRCRIS 850
Db 155 EPLASVLRKVPDFKELVLSNDDFHEAGHTILCOGLKDSACQLESKLENCIGITSANCKDL 214
QY 851 ASTLSVNSQSLRELDLSNELGDLGVLLLCCEGLRHPNCKLQNLKRCRIS 910
Db 215 CDVASKASLQELDLGSKNGKNTGIALCSGILLPSCRLRLTWLWDCDVTAGCKDL 274
QY 911 LQAHNRLDELDFNDLGDWGLWLAEGLOHPACRLQKWLWLDSCGLTAKACENLYFTLGI 970
Db 275 LRAQSKLSKLSLGNELKDEGAQLLCELSLEPGQLESWLKVTCSLTAAASCPHFCSVLTK 334
QY 971 NQTLTDLVTLNAGDGTGRLICKELSHPGCKRLVRLWLFNGMDLNKMTLSRAAL 1024
Db 335 NSSLFELQMSNPLGSDSGVWELCKALGYDPTVLRVILWLGDCDVTDSGCSLSATV 388

RESULT 9

US-08-910-731-8
; Sequence 8, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-910-731-8

Query Match 13.0%; Score 712; DB 2; Length 456;
Best Local Similarity 42.5%; Pred. No. 3.9e-61;
Matches 150; Conservative 61; Mismatches 142; Indels 0; Gaps 0;
QY 671 LLDAYSEHLAAALCTNPNIETSLYRNALSGRGVKKLCOGLRHPNCKLQNLKRCRIS 730
Db 35 LTVCKDIRSAIQANPALTELSRTNELGAGVGLVQLGQNTCKIQKLSQNCSLTE 94
QY 731 SACEDELSAALIANKNLTMRDLSGNGVFPFGMMLLCEGLRHPNCKLQNLKRCRIS 790
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RESULT 10

US-08-910-731-2
; Sequence 2, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-910-731-2

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Best Local Similarity 42.7%; Pred. No. 7.7e-61;
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US-08-795-395-2
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; Patent No. 5965399
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Cloning and Expression of Rat Liver and
; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,395
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-395-2

Query Match 13.0%; Score 709; DB 2; Length 456;
Best Local Similarity 42.7%; Pred. No. 7.7e-61;
Matches 151; Conservativity 60; Mismatches 143; Indels 0; Gaps 0;
Qy 671 LLDAYSSEHAAALCTNPNIETLSLYRNALGSRGVKLLCQGLRHPNCCKLQNLRLKRCRISS 730
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:	APPLICANT:	Ogur, Yasunori			
:	TITLE OF INVENTION:	NOD2 Nucleic Acids and Proteins			
:	FILE REFERENCE:	UM-06645			
:	CURRENT APPLICATION NUMBER:	US/10/014,269			
:	CURRENT FILING DATE:	2001-10-26			
:	NUMBER OF SEQ ID NOS:	52			
:	SOFTWARE:	PatentIn version 3.1			
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:	TYPE:	PRT			
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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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ALIGNMENTS

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DEFINITION Sequence 23 from Patent WO0226780.
ACCESSION AX417214
VERSION AX417214.1 GI:21449784
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Read, J.C., Godzik, A., Chu, Z.L., Pawlowski, K., Fiorentino, L., Ariza, M.E. and Stehlik, C.
TITLE Paad domain-containing polypeptides, encoding nucleic acids, and Methods of use
JOURNAL Patent: WO 0226780-A 23 04-APR-2002;
The Burnham Institute (US)
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DEFINITION Sequence 12 from Patent WO0240668.
ACCESSION AX459869
VERSION AX459869.1 GI:21725643
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
AUTHORS Tschoopp,J. and Martinon,F.
TITLE Proteins and dna sequences underlying these proteins used for treating inflammations
JOURNAL Patent: WO 0240668-A 12 23-MAY-2002;
Apotech Research and Development Ltd. (CH)
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RESULT 3
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LOCUS Homo sapiens monarch-1 mRNA, complete cds; alternatively spliced.
DEFINITION AY116204
ACCESSION AY116204
VERSION AY116204.1 GI:21711820
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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1 (bases 1 to 3731)
Williams,K.L., Taxman,D.J., Linhoff,M.W., Reed,W. and Ting,J.P.Y.
Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat
Protein That Controls Classical and Nonclassical MHC Class I Genes
J. Immunol. 170 (11), 5354-5358 (2003)
12759408
2 (bases 1 to 3731)
Williams,K.L., Linhoff,M.W., Harton,J.A. and Ting,J.P.Y.
Direct Submission
AUTHORS
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JOURNAL
PUBMED
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21955153.

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		Best Local Similarity 97.4%; Pred. No. 0;	
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Db		120 ATGCTACGAACCGCAGGACGCGGCTCTGTGCGCTGTCCACTTACTTGGAGAACTC 179	
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DEFINITION	Homo sapiens NACHT, leucine rich repeat and PYD containing 12, mRNA (CDNA clone MGC:40117 IMAGE:5212737), complete cds.		
ACCESSION	BC028069		
VERSION	MGC		
KEYWORDS	MGC		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3507) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 3507)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nhgri.nih.gov Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 62 Row: g Column: 10			

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Db	837	ATAGGCAAGTCCATGCTGGACACCAAGGTGATGCTGGACTGGCGGACGGAGGCTCTTC	896	Qy	1720	AGCGACGCGCTCCACCTCTGACAGCGGCTCTTGGAGTCTTTCAGCTGCTTGTACGAGATC	1779
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REFERENCE
1 (bases 1 to 3827)
Tschoep, J., Martinon, F. and Burns, K.
NALP12: a novel protein family involved in inflammation
JOURNAL Nat. Rev. Mol. Cell Biol. 4 (2), 95-104 (2003)
MEDLINE 22451042
PUBMED 12563287
REFERENCE
2 (bases 1 to 3827)
Martinon, F., Hofmann, K. and Tschopp, J.
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DEFINITION alternatively spliced.
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VERSION AY116205.1 GI:21711822
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 3563)
Williams.K.L., Taxman,D.J., Linhoff,M.W., Reed,W. and Ting,J.P.Y.
Monarch-1: A Pyrin/Nucleotide-Binding Domain/Leucine-Rich Repeat
Protein That Controls Classical and Nonclassical MHC Class I Genes
J. Immunol. 170 (11), 5354-5358 (2003)
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2 (bases 1 to 3563)
Williams.K.L., Linhoff,M.W. and Ting,J.P.Y.
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LOCUS

DEFINITION

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PAT 15-DEC-2003

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and
Maseho, Y.

TITLE Full-length cDNA sequences

Patent: EP 1347046-A 718 24-SEP-2003;

JOURNAL Research Association for Biotechnology (JP)

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ORGANISM	Homo sapiens		
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TITLE	JOURNAL		
	PUBLISHED		

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Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Negai, K. and Isogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 3 (bases 1 to 3466)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 Karusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3985)
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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ORIGIN

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REFERENCE
AUTHORS Williams, K.L., Taxman, D.J., Linhoff, M.W., Reed, W. and Ting, J.P.Y.
TITLE Monarch-1: A Pyrim/Nucleotide-Binding Domain/Leucine-Rich Repeat Protein That Controls Classical and Nonclassical MHC Class I Genes
J. Immunol. 170 (11), 5354-5358 (2003)
JOURNAL
PUBMED 12759408
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AUTHORS Williams, K.L., Linhoff, M.W. and Ting, J.P.Y.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Thornton.M., Hafalia,A.J., Lu,D.A., Arvizu,C., Swarnakar,A., Lu,Y.,
Warren,B.A., Baughn,M.R., Tang,Y.T., Lee,E.A., Yao,M.G.,
Ranikumar,J., Khan,F.A., Gandhi,A.R., Ding,L., Yue,H., Gietzen,K.J.,

Walia,N.K., Thangavelu,K., Elliot,V.S. and Marquis,J.P.
Nucleic acid-associated proteins
Patent: WO 02072630-A 19 19-SEP-2002;
Incyte Genomics, Inc. (US)
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DEFINITION Sequence 1 from Patent WO02052011.
ACCESSION AX684291
VERSION AX684291.1 GI:29371161
KEYWORDS Homo sapiens (human)
SOURCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Feder, J., Ramanathan, C. and Mintier, G.

TITLE Human leucine-rich repeat containing protein, hlrhbm1, expressed
predominately in bone marrow
JOURNAL Patent: WO 02052011-A 1 04-JUL-2002;
Bristol-Myers Squibb Company (US)
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ORIGIN

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AC150815
LOCUS
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unordered pieces.
ACCSSION
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SOURCE Callithrix jacchus (white-tufted-ear marmoset)
ORGANISM Callithrix jacchus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix. 1 (bases 1 to 202418) Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A., Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H., Engle,J., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurlb,B., Idoi,J.R., Jones,C., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-O., Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J., Mullikin,J.C., Oestreich,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O., Reddix-Dugue,N., Rosas,B., Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Stephen,E., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and Green,E.D. NSC Comparative Sequencing Initiative Unpublished 2 (bases 1 to 202418) Green,E.D. Direct Submission Submitted (11-AUG-2004) NIH Intramural Sequencing Center, 8717 Government Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 202418) Green,E.D. Direct Submission Submitted (13-OCT-2004) NIH Intramural Sequencing Center, 8717 Government Circle, Gaithersburg, MD 20877, USA On Oct 13, 2004 this sequence version replaced gi:51101019. ----- Genome Center Center: NIH Intramural Sequencing Center Center code: NSIC Web site: http://www.nisc.nih.gov Contact: nisc.zoo@nhgri.nih.gov ----- Project Information Center project name: hle Center clone name: 282L08 ----- Summary Statistics Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 184606 bases at least Q40 Consensus quality: 186962 bases at least Q30 Consensus quality: 188671 bases at least Q20 Insert size: 200000; agarose-fp Insert size: 200618; sum-of-contigs Quality coverage: 8.1x in Q20 bases; agarose-fp Quality coverage: 8.1ix in Q20 bases; sum-of-contigs ----- * NOTE: This is a 'working draft' sequence. It currently * consists of 19 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.		
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AUTHORS	* 32667	39814: contig of 7048 bp in length
JOURNAL	* 39815	39914: gap of unknown length
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 3108

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Searched: 4390206 seqs, 2959870667 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	3017	97.1	3731	12 ADP47723	Adp47723 Human Mon
5	2997.8	96.5	3186	6 AAL44363	Aal44363 Human PYR
6	2997.8	96.5	3186	10 ADP47754	Adp47754 Human PYR
7	2929	94.2	3218	12 ADJ19382	Adj19382 Human PAN
8	2759	88.8	3563	12 ADP47725	Adp47725 Human Mon
9	2644.2	85.1	3466	11 ADM02033	Adm02033 Human cDN
10	2470	79.5	3395	12 ADP47727	Adp47727 Human Mon
11	2449.4	78.8	3305	10 ADC30316	Adc30316 Human nov
12	2417	77.0	3221	12 ADP47729	Adp47729 Human Mon
13	1864.8	60.0	3102	12 ADP47731	Adp47731 Murine Mo
14	1705.4	54.9	1800	8 ACD03623	Acd03623 Novel hum
15	1681.8	54.1	2158	6 ABS78719	Abs78719 Human cDN
16	1680	54.1	1704	12 ACH91465	Ach91465 Human gen
17	1616	52.0	4931	6 ABL59333	Ab159333 Nucleotid
18	1491.4	48.0	1684	12 ADM93802	Adm93802 DNA encod
19	1394.8	44.9	1682	12 ADM93804	Adm93804 DNA encod
20	1394.8	44.9	1683	8 ACD03624	Acd03624 Novel hum

21	803.6	25.9	2835	12 ADP47755	Adp47755 Human CAT
22	803.6	25.9	4170	13 ADP24013	Adp24013 PRO polyp
23	803.6	25.9	4344	11 ADM34349	Adm34349 Human cry
24	800.4	25.8	3857	4 AAD14323	Aad14323 Human PYR
25	800.4	25.8	3857	9 ABX93556	Abx93556 Huma cDNA
26	800.4	25.8	3857	9 ACD27909	Acd27909 Human PYR
27	783.2	25.2	2934	12 ADP47869	Adp47869 Human CAT
28	640.6	20.6	2154	12 ADP47753	Adp47753 Human CAT
29	639	20.6	2524	6 ADE36451	Ade36451 Human PAA
30	639	20.6	2524	12 ADJ19373	Adj19373 Human PAN
31	626.6	20.2	2546	10 ADF81910	Adf81910 Leukaemia
32	594.6	19.1	2847	4 AAS01487	Aas01487 Human sec
33	594.6	19.1	2847	8 ABZ73494	Abz73494 Secreted
34	594.6	19.1	2847	8 ADA98038	Ada98038 Human sec
35	594.6	19.1	2847	10 ADC20194	Adc20194 Human sec
36	594.6	19.1	2847	10 ADF10619	Adf10619 Human sec
37	588.4	18.9	591	10 ADC32201	Adc32201 Human nov
38	509	16.4	509	12 ACH77762	Ach77762 Human gen
39	478.6	15.4	3039	12 ADP47733	Adp47733 Human inf
40	477.8	15.4	506	5 AAS68757	Aas68757 DNA encod
41	470.4	15.1	1557	6 AAL47143	Aal47143 Pyrin dom
42	456	14.7	2808	12 ADP47735	Adp47735 Human inf
43	453.4	14.6	487	9 ACH36225	Ach36225 Human end
44	450.8	14.5	479	3 AAC76566	Aac76566 Human ORF
45	438.4	14.1	2775	12 ADO50889	Ado50889 Human NOV

ALIGNMENTS

RESULT 1

ADE36416

ID ADE36416 standard; cDNA; 3108 BP.

XX ADE36416;

XX 29-JAN-2004 (first entry)

XX Human PAA and nucleotide binding protein PAN6 cDNA.

XX cytosolic; immunosuppressive; vulnary; antiinflammatory; vasotropic;
XX antiallergic; antiulcer; dermatological; cerebroprotective; cardiac;
XX antiparkinsonian; nootropic; neuroprotective; anti-HIV; gene therapy;
XX NFkappaB activation inhibitor; PAA domain containing polypeptide;
XX PAA and nucleotide binding protein 2-6; PAN 2-6; pyrin 2;
XX apoptosis-associated speck-like protein; caspase recruitment domain 2;
XX ASC-2; nuclear factor kappa B activation inhibitor; NB-ARC domain;
XX apoptosis; NFkappaB induction; cytokine processing;
XX cytokine receptor signaling caspase-mediated proteolysis;
XX c-Jun N-terminal kinase activation; cell life; cell death; apoptosis;
XX inflammation; cell adhesion; cancer; keratinocyte; hyperplasia;
XX neoplasia; keloid benign prostatic hypertrophy; inflammatory hyperplasia;
XX fibrosis; smooth muscle cell proliferation; balloon angioplasty;
XX restenosis; leukaemia; lymphoma; inflammatory disease; allergy;
XX arthritis; lupus; schrojen's syndrome; Crohn's disease;
XX ulcerative colitis; graft versus host disease; stroke; heart failure;
XX neurodegenerative disease; parkinson's disease; Alzheimer's disease; HIV;
XX cancer therapy; PAA domain family; human; PAN6; gene; ss.

OS Homo sapiens.

XX US2003077699-A1.

XX 24-APR-2003.

XX 25-SEP-2001; 2001US-00965621.

XX 26-SEP-2000; 2000US-00671760.

XX 26-SEP-2000; 2000US-0367367P.

XX (REED)/ REED J C.

XX (GODZ)/ GODZIK A.

XX (CHUZ)/ CHU Z.

[illegible]

PS	Example; SEQ ID NO 23; 193pp; English.	
xx	The invention relates to a novel isolated nucleic acid molecule encoding	
CC	a PAAD-containing polypeptide. The polypeptide of the invention	
CC	demonstrates cytosolic activity and may be useful for preparing a	
CC	composition for diagnosing or treating diseases associated with the PAAD	
CC	domain-containing polypeptide, such as cancer, via gene therapy. The	
CC	current sequence is that of the human PAAD domain-containing protein full	
xx	-length cDNA of the invention.	
SQ	Sequence 3108 BP; 682 A; 883 C; 931 G; 612 T; 0 U; 0 Other;	
Query Match	100.0%; Score 3108; DB 12; Length 3108;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 3108; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGCTACGAACCGCAGGAGCGGCTCTGTGCGCTGTCCACCTACTTTGGAAGAACTC 60	Db
DB	1 ATGCTACGAACCGCAGGAGCGGCTCTGTGCGCTGTCCACCTACTTTGGAAGAACTC 60	
QY	61 GAGGCTGTGAACTGAAGAAGTTCAAGTTATACCTGGGGACCGGACAGAGCTGGGAGAA 120	
DB	61 GAGGCTGTGAACTGAAGAAGTTCAAGTTATACCTGGGGACCGGACAGAGCTGGGAGAA 120	
QY	121 GCGAAGATCCCTCGGGAGCATGGAAGCGCGTCCCTCGGAATGGGCCACAGCTGCTC 180	
DB	121 GCGAAGATCCCTCGGGAGCATGGAAGCGCGTCCCTCGGAATGGGCCACAGCTGCTC 180	
QY	181 ATCAACCCATTCGGGCCAGAGGAGCGCTGTGAGGTGGCTCTCAGCACTTTGAGCGGATA 240	
DB	181 ATCAACCCATTCGGGCCAGAGGAGCGCTGTGAGGTGGCTCTCAGCACTTTGAGCGGATA 240	
QY	241 AACAGGAAGCACTGTGGGAGAGGACAGAGAGCACTGTGTGGGATCCCGAGGAA 300	
DB	241 AACAGGAAGCACTGTGGGAGAGGACAGAGAGCACTGTGTGGGATCCCGAGGAA 300	
QY	301 ACCTACAGGAGTATGTCGCGAGAAATTCGGGCTCATGGAAGACCGCAATGGCGGCTTA 360	
DB	301 ACCTACAGGAGTATGTCGCGAGAAATTCGGGCTCATGGAAGACCGCAATGGCGGCTTA 360	
QY	361 GGGGAATGTCAACCTCAGCCACCGGTAACACCGGCTCTGTGTGTGAAGGAGCACTCA 420	
DB	361 GGGGAATGTCAACCTCAGCCACCGGTAACACCGGCTCTGTGTGTGAAGGAGCACTCA 420	
QY	421 AACCCCATGAGTCCAGCAGCTTCTGGACACAGCCGGGACACGCGAGGACCGTG 480	
DB	421 AACCCCATGAGTCCAGCAGCTTCTGGACACAGCCGGGACACGCGAGGACCGTG 480	
QY	481 GGACACCAAGGCTAGCCCATCAAGATAGAGACCCCTTTTGAAGCAGAGGAGCGGCC 540	
DB	481 GGACACCAAGGCTAGCCCATCAAGATAGAGACCCCTTTTGAAGCAGAGGAGCGGCC 540	
QY	541 GAGCCACCGCGACCGTGGTATGCAAGCGCGGAGGGATAGGCAAGTCCATCTGGCA 600	
DB	541 GAGCCACCGCGACCGTGGTATGCAAGCGCGGAGGGATAGGCAAGTCCATCTGGCA 600	
QY	601 CACAGGTTGATCTGCTGCTGGCGGACGGGAAGCTCTTCCAAAGGAGATTTGATTATCTC 660	
DB	601 CACAGGTTGATCTGCTGCTGGCGGACGGGAAGCTCTTCCAAAGGAGATTTGATTATCTC 660	
QY	661 TTCTACATCAACTGAGGAGATGAACCAAGATGTCACCGAATGCAGATCAAGACTTC 720	
DB	661 TTCTACATCAACTGAGGAGATGAACCAAGATGTCACCGAATGCAGATCAAGACTTC 720	
QY	721 ATCTTACGCTGTGCTGAGCCAGCGGCTCTCCAGGAGCTCATCCGAGTTCCCGAG 780	
DB	721 ATCTTACGCTGTGCTGAGCCAGCGGCTCTCCAGGAGCTCATCCGAGTTCCCGAG 780	
QY	781 CGCTCTCTTTTCATCATCAAGCGGCTTCGATGAGCTCAAGGCTCTTTCCAGGATCCTCAG 840	
DB	781 CGCTCTCTTTTCATCATCAAGCGGCTTCGATGAGCTCAAGGCTCTTTCCAGGATCCTCAG 840	
QY	841 GGACCCCTGTGCTCTGTGGGAGGAGAAACGGGCCACGAGAGCTGCTTTAAAGCTTA 900	

841	GGACCCCTGTGCTCTGTGGAGGAGAAACGGGCCACGAGCTGCTCTTTAAAGCTTA 900	Db
901	ATTGGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACACAGGCCCCACGGCTTTG 960	QY
901	ATTGGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACACAGGCCCCACGGCTTTG 960	Db
961	GAGAAAGTCCACCGCTGCTGTGAGCACCACAGGATGTGGAGATCTCTGGGCTTTCTGAG 1020	QY
961	GAGAAAGTCCACCGCTGCTGTGAGCACCACAGGATGTGGAGATCTCTGGGCTTTCTGAG 1020	Db
1021	GCAGAAAGGAAGGAATACTTTCAAGATTTTCAATGAGAGCAGCGGGCCCAAGTC 1080	QY
1021	GCAGAAAGGAAGGAATACTTTCAAGATTTTCAATGAGAGCAGCGGGCCCAAGTC 1080	Db
1081	TTCAATTAAGTGAAGGACCAAGAGCTCTTTCAATGCTGCTGCTCCCTGCTGCTGTC 1140	QY
1081	TTCAATTAAGTGAAGGACCAAGAGCTCTTTCAATGCTGCTGCTCCCTGCTGCTGTC 1140	Db
1141	TGGGTGTGTGTACCTGCTCCAGCAGCAGCTGGAGGTGGGGCTGTGTGAGACAGACG 1200	QY
1141	TGGGTGTGTGTACCTGCTCCAGCAGCAGCTGGAGGTGGGGCTGTGTGAGACAGACG 1200	Db
1201	TTCCAGAACCAACACTGCTGCTGCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260	QY
1201	TTCCAGAACCAACACTGCTGCTGCTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260	Db
1261	GGGGCCCGCGCTCCAGCCCAACCAAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1320	QY
1261	GGGGCCCGCGCTCCAGCCCAACCAAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1320	Db
1321	GGGCTCTGGAATCAGAAATCTATTTGAGGAGCAGGACCTCCGGAAGCAGCGGCTTAGAC 1380	QY
1321	GGGCTCTGGAATCAGAAATCTATTTGAGGAGCAGGACCTCCGGAAGCAGCGGCTTAGAC 1380	Db
1381	GGGGAAGAGCTCTGCTGCTTCTCAACATGACATCTTCCAGAGACATCAACTGTGAG 1440	QY
1381	GGGGAAGAGCTCTGCTGCTTCTCAACATGACATCTTCCAGAGACATCAACTGTGAG 1440	Db
1441	AGGTACTACAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500	QY
1441	AGGTACTACAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500	Db
1501	CTGGAACGAGGGGAGGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1560	QY
1501	CTGGAACGAGGGGAGGGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1560	Db
1561	TAGCGCTTTTCTGAAAGGAGCTTCTGCGCACTCAGCAGCGCTTCTGCTGCTGCTGCTG 1620	QY
1561	TAGCGCTTTTCTGAAAGGAGCTTCTGCGCACTCAGCAGCGCTTCTGCTGCTGCTGCTG 1620	Db
1621	AACGAGGAGACCAAGGAGCCACTTGGAGAGAGTCTCTGTGGAAGTCTCGCGGCAATC 1680	QY
1621	AACGAGGAGACCAAGGAGCCACTTGGAGAGAGTCTCTGTGGAAGTCTCGCGGCAATC 1680	Db
1681	AAGATGGAACCTGTTGAGTGGATCCAAAGCAAGCTCAGAGCGGCTCCACCTGCGAG 1740	QY
1681	AAGATGGAACCTGTTGAGTGGATCCAAAGCAAGCTCAGAGCGGCTCCACCTGCGAG 1740	Db
1741	CAGGGCTCTCTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800	QY
1741	CAGGGCTCTCTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800	Db
1801	CAGGCCCTGAGCACTTCCAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1860	QY
1801	CAGGCCCTGAGCACTTCCAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1860	Db
1861	ATGGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920	QY
1861	ATGGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920	Db
1921	GCCACCTTACAGCGCGGAGGAGACCGCGGAGGTGCTCCGAGAGGCGACACGCTG 1980	QY

Db 1921 GCCACCTTACAGCGGGAAGACCGCGGAGGTGCTCCGAGGAGGCCACACGCTG 1980
Qy 1981 TTGGTGACGCTCAGACACAGAGAGACCGTCTTCTGTGACGCTTACAGTGAACATCTGGCA 2040
Db 1981 TTGGTGACGCTCAGACACAGAGAGACCGTCTTCTGTGACGCTTACAGTGAACATCTGGCA 2040
Qy 2041 CGGGCCCTGTGCAACCAATCCAACTGATAGAGTGTCTGTATCCGAAATGCCCTGGGC 2100
Db 2041 CGGGCCCTGTGCAACCAATCCAACTGATAGAGTGTCTGTATCCGAAATGCCCTGGGC 2100
Qy 2101 AGCCGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACCCCACTGCAAACTTCAGAAC 2160
Db 2101 AGCCGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACCCCACTGCAAACTTCAGAAC 2160
Qy 2161 CTGAGGCTGAAGAGGTGCGCATCTCCAGCTCAGCTCGAGGACCTCTCTGACGCTCTC 2220
Db 2161 CTGAGGCTGAAGAGGTGCGCATCTCCAGCTCAGCTCGAGGACCTCTCTGACGCTCTC 2220
Qy 2221 ATAGCCAAATGAATTTGACAAGATGGATCTCAGTGGCAACGGGGTTGGATTTCCAGGC 2280
Db 2221 ATAGCCAAATGAATTTGACAAGATGGATCTCAGTGGCAACGGGGTTGGATTTCCAGGC 2280
Qy 2281 ATGATGCTGCTTTCGGAGGCTCGGCATCCCGAGTCCAGCTGCAGATGATTCAGTTG 2340
Db 2281 ATGATGCTGCTTTCGGAGGCTCGGCATCCCGAGTCCAGCTGCAGATGATTCAGTTG 2340
Qy 2341 AGGAAGTGTGAGTGTGCGGGCTTGTGAGAGATGGCTTCTGTGCTCGGACCAAC 2400
Db 2341 AGGAAGTGTGAGTGTGCGGGCTTGTGAGAGATGGCTTCTGTGCTCGGACCAAC 2400
Qy 2401 CCACATCTGTTGAGTTGGACCTGACAGGAATGCATCGAGGATTTGGGCTCAGGTTA 2460
Db 2401 CCACATCTGTTGAGTTGGACCTGACAGGAATGCATCGAGGATTTGGGCTCAGGTTA 2460
Qy 2461 CTATGCCAGGACTGAGGACCCAGTCTGAGACTTTCGAGACTTTCGAGTGAAGATCTGC 2520
Db 2461 CTATGCCAGGACTGAGGACCCAGTCTGAGACTTTCGAGACTTTCGAGTGAAGATCTGC 2520
Qy 2521 CGCTCACTGCTGCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2580
Db 2521 CGCTCACTGCTGCTGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2580
Qy 2581 AGAGAGTGGACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2640
Db 2581 AGAGAGTGGACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2640
Qy 2641 GGCCTCAGGATCCCACTGCAAGCTCCAGACCTCGGCTGAGCTGAGCTGAGCTGAGCTG 2700
Db 2641 GGCCTCAGGATCCCACTGCAAGCTCCAGACCTCGGCTGAGCTGAGCTGAGCTGAGCTG 2700
Qy 2701 TCTGCCGCTGTGAGGCTTCTTCTGTGTGTCTCAGGCAACCACTCCGGGAGCTG 2760
Db 2701 TCTGCCGCTGTGAGGCTTCTTCTGTGTGTCTCAGGCAACCACTCCGGGAGCTG 2760
Qy 2761 GACTTGAATTTCAACGACCTGGGAGACTGGGCTGTGGTGTCTGCTGAGGGCTGCA 2820
Db 2761 GACTTGAATTTCAACGACCTGGGAGACTGGGCTGTGGTGTCTGCTGAGGGCTGCA 2820
Qy 2821 CATCCGCTCAGACTCCAGAACTGTGGCTGTGATAGCTGTGGCTCAGACCAAGCT 2880
Db 2821 CATCCGCTCAGACTCCAGAACTGTGGCTGTGATAGCTGTGGCTCAGACCAAGCT 2880
Qy 2881 TGTGAAATCTTTACTTCACTGGGATCAACAGACTTTGACGACCTTTTACTGACC 2940
Db 2881 TGTGAAATCTTTACTTCACTGGGATCAACAGACTTTGACGACCTTTTACTGACC 2940
Qy 2941 AACACGCTTAGGGGACACAGGTGTCCGACTGCTTTTTCAGAGCGGCTGAGCCATCTGGC 3000
Db 2941 AACACGCTTAGGGGACACAGGTGTCCGACTGCTTTTTCAGAGCGGCTGAGCCATCTGGC 3000
Qy 3001 TGCAACTCCAGTCTCTGTTTATTTGGGATGAGACCTGGAATAAATGACCCACAGTAGG 3060
Db 3001 TGCAACTCCAGTCTCTGTTTATTTGGGATGAGACCTGGAATAAATGACCCACAGTAGG 3060

Qy 3061 TTGSCAGCGCTTCGAGTAACAAAACCTTATTTGGACATTGGCTGCTGA 3108
Db 3061 TTGSCAGCGCTTCGAGTAACAAAACCTTATTTGGACATTGGCTGCTGA 3108

RESULT 3

AAAL47129
ID AAL47129 standard; DNA; 3300 BP.

XX AAL47129;

XX AC AAL47129;

XX 20-AUG-2002 (first entry)

XX Pyrin domain containing protein NALP3/PY5-hs coding sequence.

XX Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
XX antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
XX neuroprotective; antiarthritic; antirheumatic; antiaesthetic;
XX nephrotropic; osteopathic; nontropic; intracellular signal transduction;
XX inflammation; Alzheimer's disease; infection; psoriasis; asthma;
XX arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
XX osteoarthritis; glomerulonephritis; gene; ds.

XX Unidentified.

XX WO200240668-A2.

XX 23-MAY-2002.

XX 30-OCT-2001; 2001WO-EP012545.

XX 15-NOV-2000; 2000DE-01056687.

XX 30-NOV-2000; 2000DE-01059595.

XX (APOT-) APOTECH RES & DEV LTD.

XX Tschopp J, Martinson F;

XX WPI; 2002-427093/45.

XX P-PSDB; AAO17857.

XX New DNA encoding protein with pyrin domain, useful for treating diseases
XX involving impaired signal transduction, particularly inflammation, also
XX proteins and antibodies.

XX Claim 5; Fig 1; 116pp; German.

XX The present invention relates the DNA and their encoded proteins, where
XX the proteins contain at least one PYD (pyrin) domain. These can be used
XX to treat diseases associated with impaired intracellular signal
XX transduction, particularly inflammation such as psoriasis,
XX arteriosclerosis, bacterial or viral infections (particularly meningitis
XX and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
XX sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
XX and Parkinson's diseases. The present sequence is a coding sequence of
XX the invention

XX Sequence 3300 BP; 726 A; 943 C; 979 G; 652 T; 0 U; 0 Other;

Query Match 98.4%; Score 3057; DB 6; Length 3300;
Best Local Similarity 100.0%; Pred.No. 0;

Matches 3057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTACGAACCCGAGCAGGACGGCTCTGTGCTGTCCACTTACTTGGAGAACTC 60

Db 1 ATGCTACGAACCCGAGCAGGACGGCTCTGTGCTGTCCACTTACTTGGAGAACTC 60

Qy 61 GAGGCTGTGAACCTGAAGAAAGTTCAAGTTATACCTGGGACCGGACAGAGCTGGGAGAA 120

Db 61 GAGGCTGTGAACCTGAAGAAAGTTCAAGTTATACCTGGGACCGGACAGAGCTGGGAGAA 120

Qy 121 GGCAAGATCCCTGGGGGAGCATGGAGAGGCGGCTCCCTTGGAAATGGCCCACTGCTC 180

Db 121 GGAAGATCCCTGGGGAAGCATGGAGAGCGCGTCCCTGGAAATGGCCAGCTGCTC 180
QY 181 ATCAACCACTTCGGGCCAGAGAGGCTGGAGGTGGCTCTCAGCACTTTGAGCGGATA 240
Db 181 ATCAACCACTTCGGGCCAGAGAGGCTGGAGGTGGCTCTCAGCACTTTGAGCGGATA 240
QY 241 AACAGGAAGACCTGTGGGAGAGAGACAGAGAGAGACCTGTGTGAGGATCCCAAGGAA 300
Db 241 AACAGGAAGACCTGTGGGAGAGAGACAGAGAGAGACCTGTGTGAGGATCCCAAGGAA 300
QY 301 ACCTACAGGACATGTCGCGAGGAATTCGCGCTCATGGAAGACCGCAATGCGCGCTTA 360
Db 301 ACCTACAGGACATGTCGCGAGGAATTCGCGCTCATGGAAGACCGCAATGCGCGCTTA 360
QY 361 GGGGAATGTGCAACCTCAGCCACCGGTACACCGGCTCTCTGTGTGAGAGAGCACTCA 420
Db 361 GGGGAATGTGCAACCTCAGCCACCGGTACACCGGCTCTCTGTGTGAGAGAGCACTCA 420
QY 421 AACCCCATGAGGTCCAGAGACAGCTTCTGGACAACAGGCCGGGACACCGGAGACCGTG 480
Db 421 AACCCCATGAGGTCCAGAGACAGCTTCTGGACAACAGGCCGGGACACCGGAGACCGTG 480
QY 481 GGACACAGGCTAGCCCATCAAGATAGAGACCTCTTTGAGCCAGACGAGGAGCGCCCC 540
Db 481 GGACACAGGCTAGCCCATCAAGATAGAGACCTCTTTGAGCCAGACGAGGAGCGCCCC 540
QY 541 GAGCCACCGCACCGTGGTCAATCAAGCGCGCGCAGGGATAGGCAAGTCCATGCTGGCA 600
Db 541 GAGCCACCGCACCGTGGTCAATCAAGCGCGCGCAGGGATAGGCAAGTCCATGCTGGCA 600
QY 601 CACAAGGTGATGCTGGACTGGAGCGGAGGATCTTCCAGGACGATTTGATTTATCTC 660
Db 601 CACAAGGTGATGCTGGACTGGAGCGGAGGATCTTCCAGGACGATTTGATTTATCTC 660
QY 661 TTCTACATCAACTGCAGGGAGATGACCCAGAGTGCACGGAATGCAGATGCAAGACCTC 720
Db 661 TTCTACATCAACTGCAGGGAGATGACCCAGAGTGCACGGAATGCAGATGCAAGACCTC 720
QY 721 ATCTTCAGCTGCTGCTGAGCCAGCGGCTCTCCAGGAGCTCATCCGAGTTCGCGAG 780
Db 721 ATCTTCAGCTGCTGCTGAGCCAGCGGCTCTCCAGGAGCTCATCCGAGTTCGCGAG 780
QY 781 GCGCTCTTTTCATCATCGAGGCTTCGATGAGCTCAAGCTTCTTCCAGATCTCTCAG 840
Db 781 GCGCTCTTTTCATCATCGAGGCTTCGATGAGCTCAAGCTTCTTCCAGATCTCTCAG 840
QY 841 GGACCTGCTGCTGCTGGAGGAGAAACGGCCACCGGAGCTGCTTTTAAACAGCTTA 900
Db 841 GGACCTGCTGCTGCTGGAGGAGAAACGGCCACCGGAGCTGCTTTTAAACAGCTTA 900
QY 901 ATTGCGAAGAGCTGCTGCTGAGCTATCTTTGCTCATCACACAGCCCAACGGCTTG 960
Db 901 ATTGCGAAGAGCTGCTGCTGAGCTATCTTTGCTCATCACACAGCCCAACGGCTTG 960
QY 961 GAGAGCTCCACCGTCTGCTGAGCACCCAGGATGAGATCTCGGCTTCTCTGAG 1020
Db 961 GAGAGCTCCACCGTCTGCTGAGCACCCAGGATGAGATCTCGGCTTCTCTGAG 1020
QY 1021 GCAGAAAGGAAGGAATCTTCAAGTATTTTCCAAATGACAGAGACGGCGGCAAGTC 1080
Db 1021 GCAGAAAGGAAGGAATCTTCAAGTATTTTCCAAATGACAGAGACGGCGGCAAGTC 1080
QY 1081 TTCAATTAGTGAGGGAACACAGCTCTTTCACCATGCTGCTCCCTCGTGTC 1140
Db 1081 TTCAATTAGTGAGGGAACACAGCTCTTTCACCATGCTGCTCCCTCGTGTC 1140
QY 1141 TGGGTGCTGTGTACCTGCTCCAGCAGAGCTGAGGAGTGGGGGCTGTGAGACAGACG 1200
Db 1141 TGGGTGCTGTGTGTACCTGCTCCAGCAGAGCTGAGGAGTGGGGGCTGTGAGACAGACG 1200
QY 1201 TCAGAGCAACCACTGACGTATACGTCTACCTGCTGAGTCTGATGCAACCCAGCGG 1260

Db 1201 TCCAGGACCACTGACGTGTACATGCTTACCTGCTGAGTCTGATGCAACCAACGCGG 1260
QY 1261 GGGGCCCGCGCTTCAGCCCCCAACCCAGAGAGGTTGTCTCTCTTGGCGGAGAT 1320
Db 1261 GGGGCCCGCGCTTCAGCCCCCAACCCAGAGAGGTTGTCTCTTGGCGGAGAT 1320
QY 1321 GGGCTCTGGAATCAGAAATCTTATTTGAGGAGCAGGACCTTCGGAAAGCAGCGGCTAGAC 1380
Db 1321 GGGCTCTGGAATCAGAAATCTTATTTGAGGAGCAGGACCTTCGGAAAGCAGCGGCTAGAC 1380
QY 1381 GGGGAAGACGCTCTGCGCTTCTCAAATGAAACATCTTCCAGAAAGACATCAACTGTGAG 1440
Db 1381 GGGGAAGACGCTCTGCGCTTCTCAAATGAAACATCTTCCAGAAAGACATCAACTGTGAG 1440
QY 1441 AGGTACTACGCTTCATCACTGAGTTTCCAGGAATCTTTGAGCTATCTGACTATATC 1500
Db 1441 AGGTACTACGCTTCATCACTGAGTTTCCAGGAATCTTTGAGCTATCTGACTATATC 1500
QY 1501 CTGAGCAGAGGGGAGGGCGGCGCAGACAGGACGTGACAGGCTGTTGACCGAG 1560
Db 1501 CTGAGCAGAGGGGAGGGCGGCGCAGACAGGACGTGACAGGCTGTTGACCGAG 1560
QY 1561 TACGGGTTTTCTGAAAGGAGCTTCTGGCACTCACAGCGCTTCTCTTTGGACTCTG 1620
Db 1561 TACGGGTTTTCTGAAAGGAGCTTCTGGCACTCACAGCGCTTCTCTTTGGACTCTG 1620
QY 1621 AACGAGGAGACGAGGAGCCTCTGGAGAGAGTCTCTGCTGGAGAGTCTCGCGCACATC 1680
Db 1621 AACGAGGAGACGAGGAGCCTCTGGAGAGAGTCTCTGCTGGAGAGTCTCGCGCACATC 1680
QY 1681 AAGATGGACCTGTTGAGTGGATCCAAAGCAAGCTCAGAGCGGCTCCACCCCTGAG 1740
Db 1681 AAGATGGACCTGTTGAGTGGATCCAAAGCAAGCTCAGAGCGGCTCCACCCCTGAG 1740
QY 1741 CAGGGCTCTTGGAGTCTTTCAGCTGCTTGTACAGATCCAGAGAGAGGATTTATCCAG 1800
Db 1741 CAGGGCTCTTGGAGTCTTTCAGCTGCTTGTACAGATCCAGAGAGAGGATTTATCCAG 1800
QY 1801 CAGGGCTCTGAGCACCTTCCAGGCTGATCTGCTGAGCAATTCCTCCAAGATGAGGAC 1860
Db 1801 CAGGGCTCTGAGCACCTTCCAGGCTGATCTGCTGAGCAATTCCTCCAAGATGAGGAC 1860
QY 1861 ATGCTCTCTGTTCTGTTGAAAGCGCTGACAGGCGCCAGGCTGCTGACTTGTATGCG 1920
Db 1861 ATGCTCTCTGTTCTGTTGAAAGCGCTGACAGGCGCCAGGCTGCTGACTTGTATGCG 1920
QY 1921 GCCACCTACAGCGGAGCGGGAAGACCGCGGAGGTGCTCCGAGAGCGCACACGCTG 1980
Db 1921 GCCACCTACAGCGGAGCGGGAAGACCGCGGAGGTGCTCCGAGAGCGCACACGCTG 1980
QY 1981 TTGCTGACGCTCAGACAGAGGACCGTTCCTGAGAGCGCTTACAGTGAACATCTGGCA 2040
Db 1981 TTGCTGACGCTCAGACAGAGGACCGTTCCTGAGAGCGCTTACAGTGAACATCTGGCA 2040
QY 2041 GCGGCGCTGTGACCAATCCAAACCTGATAGAGTCTCTGTACCGAAATGCCCTGGGC 2100
Db 2041 GCGGCGCTGTGACCAATCCAAACCTGATAGAGTCTCTGTACCGAAATGCCCTGGGC 2100
QY 2101 AGCGGGGGGTGAAGCTGCTCTCAAGGACTCAGACACCCCACTGCAAACTTCAGAAC 2160
Db 2101 AGCGGGGGGTGAAGCTGCTCTCAAGGACTCAGACACCCCACTGCAAACTTCAGAAC 2160
QY 2161 CTGAGGCTGAAGAGGTGCGCATCTCAGCTCAGCTCAGGAGACCTCTCTGAGCTCTC 2220
Db 2161 CTGAGGCTGAAGAGGTGCGCATCTCAGCTCAGCTCAGGAGACCTCTCTGAGCTCTC 2220
QY 2221 ATAGCCCAATGAAGATTTGCAAGGATGATCTCAGTGGCAACCGCGCTGGATTCGAGGC 2280
Db 2221 ATAGCCCAATGAAGATTTGCAAGGATGATCTCAGTGGCAACCGCGCTGGATTCGAGGC 2280
QY 2281 ATGATGCTGCTTTGCGAGGGCTCGGCACTCCCAAGTGCAGAGTGCAGATGATTCAGTTG 2340
Db 2281 ATGATGCTGCTTTGCGAGGGCTCGGCACTCCCAAGTGCAGAGTGCAGATGATTCAGTTG 2340


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QY 2341 AGGAAGTGTCACTCGAGTCGGGGCTTTGTTCAGGAGATGGCTTCTGTCTCGGACCAAC 2400
Db |||||
QY 2341 AGGAAGTGTCACTCGAGTCGGGGCTTTGTTCAGGAGATGGCTTCTGTCTCGGACCAAC 2400
Db |||||
QY 2401 CCACATCTGTTGAGTTGGACTGACAGAAATGACGAGGATTTGGGCTGAGGTTA 2460
Db |||||
QY 2401 CCACATCTGTTGAGTTGGACTGACAGAAATGACGAGGATTTGGGCTGAGGTTA 2460
Db |||||
QY 2461 CTATCCAGGAGTCTGAGGACCCAGTCTGCGAGACTACGAGCTTTGTGGCTGAAGATCGC 2520
Db |||||
QY 2461 CTATCCAGGAGTCTGAGGACCCAGTCTGCGAGACTACGAGCTTTGTGGCTGAAGATCGC 2520
Db |||||
QY 2521 GGCCTCACTGTGCTGCTGAGAGCTGAGCTGCGCTCAACTCTCAGTGTGAACAGAGCTG 2580
Db |||||
QY 2521 GGCCTCACTGTGCTGCTGAGAGCTGAGCTGCGCTCAACTCTCAGTGTGAACAGAGCTG 2580
Db |||||
QY 2581 AGAGAGTGGACCTGAGCTGAAATGAGCTGGGGACCTCGGGTGTCTGTGTGAG 2640
Db |||||
QY 2581 AGAGAGTGGACCTGAGCTGAAATGAGCTGGGGACCTCGGGTGTCTGTGTGAG 2640
Db |||||
QY 2641 GGCCTCAGGATCCACAGTCAAGCTCCAGACCTGCGGTTGGGATCTGCGGCTGGGC 2700
Db |||||
QY 2641 GGCCTCAGGATCCACAGTCAAGCTCCAGACCTGCGGTTGGGATCTGCGGCTGGGC 2700
Db |||||
QY 2701 TCTGCCGCTGTGAGGGTCTTTCTGTGTGTGCTCCAGGCAACCAACCTCCGGAGCTG 2760
Db |||||
QY 2701 TCTGCCGCTGTGAGGGTCTTTCTGTGTGTGCTCCAGGCAACCAACCTCCGGAGCTG 2760
Db |||||
QY 2761 GACTTGAATTTCAAGACTGGGAGACTGGGCTGTGTTGCTGGCTGAGGGCTGCA 2820
Db |||||
QY 2761 GACTTGAATTTCAAGACTGGGAGACTGGGCTGTGTTGCTGGCTGAGGGCTGCA 2820
Db |||||
QY 2821 CATCCCGCTGTCAGACTCCAGAACTGTGGCTGGATAGCTGTGGCTCACAAGCAAGCT 2880
Db |||||
QY 2821 CATCCCGCTGTCAGACTCCAGAACTGTGGCTGGATAGCTGTGGCTCACAAGCAAGCT 2880
Db |||||
QY 2881 TGTGAGAACTTTACTTCACTCCCTGGGATCAACAGACTTTGACCGACTTTTACCTGACC 2940
Db |||||
QY 2881 TGTGAGAACTTTACTTCACTCCCTGGGATCAACAGACTTTGACCGACTTTTACCTGACC 2940
Db |||||
QY 2941 AACACGCGCTAGGGACACAGGTGTCCAGTCTTTTCAAGCGGCTGAGCATCTCTGGC 3000
Db |||||
QY 2941 AACACGCGCTAGGGACACAGGTGTCCAGTCTTTTCAAGCGGCTGAGCATCTCTGGC 3000
Db |||||
QY 3001 TGCAACTCCGAGTCTCTGTTTATTTCGGATGGACCTGAATAAAATGACCCACAGT 3057
Db |||||
QY 3001 TGCAACTCCGAGTCTCTGTTTATTTCGGATGGACCTGAATAAAATGACCCACAGT 3057
Db |||||

RESULT 4
ADP47723
ID ADP47723 standard; cDNA; 3731 BP.
XX
AC ADP47723;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human Monarch-1 (CATERPILLER 19.3) full-length cDNA.
XX
KW Monarch-1; CATERPILLER 11.2; caspase recruitment domain;
KW CARD, transcription enhancer, R-binding, pyrin, lots of leucine repeat;
KW CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIAS1;
KW cold-induced autoinflammatory syndrome 1; antiinflammatory; cytostatic;
KW inflammatory disease; cancer; gene therapy; human; gene; ss; purine;
KW CATERPILLER 19.3; chromosome 19q13; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO2004034093-A2.
XX
PD 22-APR-2004.
XX
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30-APR-2003; 2003MO-US013562.
30-APR-2002; 2002US-0376626P.
(UYNC-) UNIV NORTH CAROLINA.
Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'Connor W;
Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;
WPI; 2004-348215/32.
P-PSDB; ADP47724.
New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3,
CATERPILLAR 16.2, CATERPILLER 16.2 or CIAS1 polypeptide, useful in
preparing a composition for treating inflammatory disease or cancer.
Claim 4; SEQ ID NO 1; 205pp; English.
The invention relates to a novel isolated nucleic acid encoding a Monarch
-1, CATERPILLER (CARD [caspase recruitment domain], transcription
enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2,
CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 [cold-
induced autoinflammatory syndrome 1] polypeptide comprising the amino
acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or
its fragment. The nucleic acid of the invention demonstrates
antiinflammatory and cytostatic activities and may be useful in preparing
a composition for treating an inflammatory disease or cancer, possibly
via gene therapy. The current sequence is that of the human Monarch-1
(CATERPILLER 19.3) full-length cDNA of the invention which is located on
chromosome 19q13, in the multiple sclerosis susceptibility region.
Sequence 3731 BP; 842 A; 1046 C; 1091 G; 752 T; 0 U; 0 Other;
Query Match 97.1%; Score 3017; DB 12; Length 3731;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 3108; Conservative 0; Mismatches 0; Indels 81; Gaps 1;
QY 1 ATGCTACGAAACCGCAGGACGAGCGGCTCTGTGCTGTCTCCACTTACTTGGAAAGACTC 60
Db 221 ATGCTACGAAACCGCAGGACGAGCGGCTCTGTGCTGTCTCCACTTACTTGGAAAGACTC 280
QY 61 GAGCTGTGNACTGAAGAAATTCAGTTATATCTTGGGACCGGACAGAGCTGGGAA 120
Db 281 GAGCTGTGNACTGAAGAAATTCAGTTATATCTTGGGACCGGACAGAGCTGGGAA 340
QY 121 GCGAAGATCCCTCGGGAAGCATCGAAGCGCGTCCCTGGAAATGCGCCAGCTGCTC 180
Db 341 GCGAAGATCCCTCGGGAAGCATCGAAGCGCGTCCCTGGAAATGCGCCAGCTGCTC 400
QY 181 ATCACCACCTTCGGGCGCAGAGGAGCGCTTGGAGTTGGCTCTCAGCACCTTTGAGCGGATA 240
Db 401 ATCACCACCTTCGGGCGCAGAGGAGCGCTTGGAGTTGGCTCTCAGCACCTTTGAGCGGATA 460
QY 241 AACAGGAAGNCTGTGGGAGAGGAGGACAGAGAGGACCTTGGTGAGG----- 288
Db 461 AACAGGAAGNCTGTGTGGGAGAGGAGGACAGAGAGGACCTTGGTGAGGAGATACCCACCT 520
QY 289 ----- 288
Db 521 GGTGGCGGCTCTCATTGGGAACCACTGAACATGCTTCTTGGAAAGTCTCTTGTGTCACT 580
QY 289 -----GATCCCCAGGAAACCTACAGGAGCTATGTCCGACAGAAATTCGGGTCTATG 339
Db 581 CCAAGAAAAGATATCCAGGAAACCTACAGGAGCTATGTCCGACAGAAATTCGGGTCTATG 640
QY 340 GAAAGCCGCAATGCGGCTTATGGGAAATGTGTCAACTCAGCACCGGATACACCCGGCTC 399
Db 641 GAAAGCCGCAATGCGGCTTATGGGAAATGTGTCAACTCAGCACCGGATACACCCGGCTC 700
QY 400 CTGCTGTGTGAGGAGGACACTCAAAACCCATGAGGTCCAGAGCAGAGCTTCTTGACACAGGC 459
Db 701 CTGCTGTGTGAGGAGGACACTCAAAACCCATGAGGTCCAGAGCAGAGCTTCTTGACACAGGC 760
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Db 2921 GGGGTGCTGCTGTGTGAGGGCTCAGGCATCCACGTGCAAGCTCCAGACCTCGG 2980
Qy 2680 TTGGGCATCTGCGGCTGGGCTCTGCCCGCTGTGAGGCTCTTTCTGTGGTCTCAGGCC 2739
Db 2981 TTGGGCATCTGCGGCTGGGCTCTGCCCGCTGTGAGGCTCTTTCTGTGGTCTCAGGCC 3040
Qy 2740 AACACAACCTCCGGAGCTGACTTGAGTTTCAACGACCTGGGAGACTGGGGCTGTGG 2799
Db 3041 AACACAACCTCCGGAGCTGACTTGAGTTTCAACGACCTGGGAGACTGGGGCTGTGG 3100
Qy 2800 TTGCTGGCTGAGGGCTCAACATCCCGCTGCAGACTCCAGAACTGTGGCTGGATAGC 2859
Db 3101 TTGCTGGCTGAGGGCTCAACATCCCGCTGCAGACTCCAGAACTGTGGCTGGATAGC 3160
Qy 2860 TGTGGCTCACAGCAAGCTTGTGAGAACTTTTACTTTCACCTCGGGATCAACAGACC 2919
Db 3161 TGTGGCTCACAGCAAGCTTGTGAGAACTTTTACTTTCACCTCGGGATCAACAGACC 3220
Qy 2920 TTGACCGACCTTACCTGACCAACACCGCTTAGGGGACAGGTGTCGACTGCTTTC 2979
Db 3221 TTGACCGACCTTACCTGACCAACACCGCTTAGGGGACAGGTGTCGACTGCTTTC 3280
Qy 2980 AAGCGCTGAGCCATCTCGGCTGCAAACTCCGAGTCTCTGTTATTGGAATGACCTG 3039
Db 3281 AAGCGCTGAGCCATCTCGGCTGCAAACTCCGAGTCTCTGTTATTGGAATGACCTG 3340
Qy 3040 AATAAATGACCCACAGTAGTGTGGCAGCGCTTCGAGTAACAAACCTTATTGGAATT 3099
Db 3341 AATAAATGACCCACAGTAGTGTGGCAGCGCTTCGAGTAACAAACCTTATTGGAATT 3400
Qy 3100 GGCTGCTGA 3108
Db 3401 GGCTGCTGA 3409

RESULT 5
AAL44363
ID AAL44363 standard; cDNA; 3186 BP.
XX
AC AAL44363;
XX
DT 31-OCT-2002 (first entry)
XX
DE Human PYRIN-8 cDNA sequence #2.
XX
KW Human; gene; ss; gene therapy; PYRIN; stress-related response;
KW apoptotic response; inflammatory response; inflammatory disorder;
KW immune system disorder; Crohn's disease; multiple sclerosis; cancer;
KW leukaemia; autoimmune disorder; arthritis; neurological disease;
KW Alzheimer's disease; Parkinson's disease; chromosomal mapping;
KW tissue typing; forensic biology; predictive medicine; pharmacogenomics;
KW transcription profiling; PYRIN-8.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..3186
FT /*tag= a
FT /product= "Human PYRIN-8 protein #2"
XX
FN WO200261049-A2.
XX
PD 08-AUG-2002.
XX
PF 31-JAN-2002; 2002WO-US002967.
XX
PR 31-JAN-2001; 2001US-0265231P.
PR 10-SEP-2001; 2001US-0318645P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PA (AMHP) WYETH.
XX
PI Bertin J, Wang W, Blatcher M;
```

XX

WPI; 2002-627477/67.

P-PSDB; AAO15590.

XX

New PYRIN polypeptides and nucleic acids useful for modulating and diagnosing stress-related, apoptotic and inflammatory responses, or for treating inflammatory and immune system disorders, cancers, or neurological diseases.

XX

Claim 4; Fig 8; 167pp; English.

PS

The invention comprises the amino acid and coding sequences of human PYRIN proteins. The PYRIN protein and DNA sequences of the invention are useful for modulating and diagnosing stress-related, apoptotic and inflammatory responses. The PYRIN protein and DNA sequences are useful for treating inflammatory disorders and immune system disorders (e.g. Crohn's disease, reactive arthritis, multiple sclerosis, contact dermatitis, psoriasis, graft rejection, allergies, viral infections and bacterial infections); cancer (e.g. leukaemia); autoimmune disorders (e.g. systemic lupus erythematosus and arthritis); and neurological diseases (e.g. Alzheimer's disease and Parkinson's disease). The PYRIN protein and DNA sequences may also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic assays, clinical trials and pharmacogenomics) and transcription profiling. The present DNA sequence encodes a human PYRIN-8 protein

XX

Sequence 3186 BP; 701 A; 908 C; 945 G; 632 T; 0 U; 0 Other;

SQ

Query Match 96.5%; Score 2997.8; DB 6; Length 3186;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 3103; Conservative 0; Mismatches 2; Indels 84; Gaps 2;

Qy

1 ATGCTACGACCCGAGGAGCGGCTCTGTGCGCTGTCCACTTCTGGAAGAACTC 60

Db

1 ATGCTACGACCCGAGGAGCGGCTCTGTGCGCTGTCCACTTCTGGAAGAACTC 60

Qy

61 GAGGCTGTGGAAGTTCAGGTTATACCTGGGGAGCCGCGACAGAGCTGGGAA 120

Db

61 GAGGCTGTGGAAGTTCAGGTTATACCTGGGGAGCCGCGACAGAGCTGGGAA 120

Qy

121 GCGAAGATCCCTGGGGAAGCATGGAGAGCCGCTCCCTGGAATGGCCAGCTGCT 180

Db

121 GCGAAGATCCCTGGGGAAGCATGGAGAGCCGCTCCCTGGAATGGCCAGCTGCT 180

Qy

181 ATACCCACATTCGGGCCAGAGAGGCTGGAGGTTGGCTCTCAGCACCTTTGAGCGGATA 240

Db

181 ATACCCACATTCGGGCCAGAGAGGCTGGAGGTTGGCTCTCAGCACCTTTGAGCGGATA 240

Qy

241 AACAGGAAGACCTGTGGGAGAGAGGACAGAGAGGACCTGTGTGAGG----- 288

Db

241 AACAGGAAGACCTGTGGGAGAGAGGACAGAGAGGACCTGTGTGAGGATACCCACCT 300

Qy

289 ----- 288

Db

301 GGTGGCCGCTCTCCTCACTTGGGAACCACTCAACATGCCTTCTGGAAGTCTCTCTTGTCACT 360

Qy

289 -----CATCCCAAGGAACCTACAGGACTATGTCCGACGAAATTCGGGCTCATG 339

Db

361 CCAAGAAAATATCCCAAGGAACCTACAGGACTATGTCCGACGAAATTCGGGCTCATG 420

Qy

340 GAAGACCGCAATGCGCGCTTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCGGCTC 399

Db

421 GAAGACCGCAATGCGCGCTTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCGGCTC 480

Qy

400 CTGCTGTGTAAGGAGCACTCAAAACCCCATGCGGTCCAGCAGCAGCTTCTGGACACAGGC 459

Db

481 CTGCTGTGTAAGGAGCACTCAAAACCCCATGCGGTCCAGCAGCAGCTTCTGGACACAGGC 540

Qy

460 CGGGGACACGGGAGGACCTGGGACACCAAGCTAGCCCCATCAAGATAGAGACCTCTTT 519

Db

541 CGGGGACACGGGAGGACCTGGGACACCAAGCTAGCCCCATCAAGATAGAGACCTCTTT 600

Qy	520	GAGCCAGACGAGAGCGCCCGAGCCACCGCGCACCGTGTGTCATGCAAGCGCGCGAGGG	579	1681	CGCTTCCTGTTTGGACTCCTGAAACGAGGAGACCCAGGAGCCACTTGGAGAAAGTCTCTGC	1740
Db	601	GAGCCAGACGAGAGCGCCCGAGCCACCGCGCACCGTGTGTCATGCAAGCGCGCGAGGG	660	1660	TGGAAGGTCTCCGCCGCACATCAAGATGACCTGTTCAGTGGATTCAAAGCAAAAGTCTAG	1719
Qy	580	ATAGGCAAGTCCATGCTGGCACACAAAGGTGATGCTGACTGGCGGAGCGGAAGTCTTTC	639	1741	TGGAAGGTCTCCGCCGCACATCAAGATGACCTGTTCAGTGGATTCAAAGCAAAAGTCTAG	1800
Db	661	ATAGGCAAGTCCATGCTGGCACACAAAGGTGATGCTGACTGGCGGAGCGGAAGTCTTTC	720	1720	AGCGACGGCTCCACCCCTCAGCAGGGCTCCTTTGAGTTCCTTTCAGTCTGTTGACGAGATC	1779
Qy	640	CAAGGACAGATTTGATTTATCTTCTTACATCAACTGCAAGGAGATGAAACGAGATGCCACG	699	1801	AGCGACGGCTCCACCCCTCAGCAGGGCTCCTTTGAGTTCCTTTCAGTCTGTTGACGAGATC	1860
Db	721	CAAGGACAGATTTGATTTATCTTCTTACATCAACTGCAAGGAGATGAAACGAGATGCCACG	780	1780	CAGGAGGAGAGTTTATCCAGCAGCGCCCTGAGCCACTTCCAGGTGATCTGGTTCAGCAAC	1839
Qy	700	GAATGACAGATGCAAGACCTCATCTTCAGTCTGGCTGAGCCAGCGCGCTCTCCAG	759	1861	CAGGAGGAGAGTTTATCCAGCAGCGCCCTGAGCCACTTCCAGGTGATCTGGTTCAGCAAC	1920
Db	781	GAATGACAGATGCAAGACCTCATCTTCAGTCTGGCTGAGCCAGCGCGCTCTCCAG	840	1840	ATTGCCCTCCAAAGATGAGCAATGCTCTCCCTGTTCTCTGTTCTGTTGAAGCGCTGCAGGAGCGCC	1899
Qy	760	GAGCTCATCCGAGTCCCGAGCGCTCCTTTTTCATCATCGACGGCTTCGATGAGCTCAAG	819	1921	ATTGCCCTCCAAAGATGAGCAATGCTCTCCCTGTTCTCTGTTCTGTTGAAGCGCTGCAGGAGCGCC	1980
Db	841	GAGCTCATCCGAGTCCCGAGCGCTCCTTTTTCATCATCGACGGCTTCGATGAGCTCAAG	900	1900	CAGGTGCTGCATTTGATGCGCCACCTTACAGCGCGGACGGGGAAGACCGCGCGAGGTGC	1959
Qy	820	CCTTCTTTCCACGATCCTCAGGAGACCTGGTGCTCTGCTGGGAGAGAAACGGCCACG	879	1981	CAGGTGCTGCATTTGATGCGCCACCTTACAGCGCGGACGGGGAAGACCGCGCGAGGTGC	2040
Db	901	CCTTCTTTCCACGATCCTCAGGAGACCTGGTGCTCTGCTGGGAGAGAAACGGCCACG	960	1960	TCGCGAGGACGACACGCTGTGTTGTCAGCTCAGACAGAGAGACCGTTCCTCTCTGGAC	2019
Qy	880	GAGCTGCTTTTAAACAGCTTAATTCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATC	939	2041	TCGCGAGGACGACACGCTGTGTTGTTGTCAGCT---ACAGAGAGGACCGTTCCTCTCTGGAC	2097
Db	961	GAGCTGCTTTTAAACAGCTTAATTCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATC	1020	2020	GCCTACAGTGAACATCTGCGAGCGGCCCTGTGTCACCAATCCAAACCTGATAGAGCTGTCT	2079
Qy	940	ACCACAGGCCACGGCTTTGGAGAGCTCCACCGTCTGCTGGAGCACCCAGGACATGTG	999	2098	GCCTACAGTGAACATCTGCGAGCGGCCCTGTGTCACCAATCCAAACCTGATAGAGCTGTCT	2157
Db	1021	ACCACAGGCCACGGCTTTGGAGAGCTCCACCGTCTGCTGGAGCACCCAGGACATGTG	1080	2080	CTGTACCGAAATGCTTGGGACGCGCGGGGGTGAAGCTGCTCTGTCTAAGAGCTCAGACAC	2139
Qy	1000	GAGATCCTGGGCTTCTCTGAGGAGAAAGAGATTAATCTTACAGTATTTTCCAAAT	1059	2158	CTGTACCGAAATGCTTGGGACGCGCGGGGGTGAAGCTGCTCTGTCTAAGAGCTCAGACAC	2217
Db	1081	GAGATCCTGGGCTTCTCTGAGGAGAAAGAGATTAATCTTACAGTATTTTCCAAAT	1140	2140	CCCAACTGCAAACTTCAGAACCTGAGCTGAAGAGGTGCCGATCTCCAGCTCAGCCTGC	2199
Qy	1060	GCAGAGCGGGCGCAAGTCTTCAATACGTGAGGAGCAACGAGCTCTCTTCCACCATG	1119	2218	CCCAACTGCAAACTTCAGAACCTGAGCTGAAGAGGTGCCGATCTCCAGCTCAGCCTGC	2277
Db	1141	GCAGAGCGGGCGCAAGTCTTCAATACGTGAGGAGCAACGAGCTCTCTTCCACCATG	1200	2200	GAGGACCTCTCTGACGCTCTCATAGCCAAATAGAAATTTGCAAGGATGATCTCAGTGGC	2259
Qy	1120	TGCTTCGTCCTCCCTGGTGTGCTGGTGTGTGCTGCTCCAGGAGAGCTGAGGGT	1179	2278	GAGGACCTCTCTGACGCTCTCATAGCCAAATAGAAATTTGCAAGGATGATCTCAGTGGC	2337
Db	1201	TGCTTCGTCCTCCCTGGTGTGCTGGTGTGTGCTGCTCCAGGAGAGCTGAGGGT	1260	2260	AAAGCGGTTGATTTCCAGGCATGCTGCTTTGCGAGGGCTCGCGGATCCCAAGTGC	2319
Qy	1180	GGGGGGCTGTGAGACAGACGTCCAGGACCAACCTGCAAGTGTACATGCTTCACTGCTG	1239	2338	AAAGCGGTTGATTTCCAGGCATGCTGCTTTGCGAGGGCTCGCGGATCCCAAGTGC	2397
Db	1261	GGGGGGCTGTGAGACAGACGTCCAGGACCAACCTGCAAGTGTACATGCTTCACTGCTG	1320	2320	AGGCTGACAGATGATTCAGTTGAGGAAGTGTGAGTTCGGGGCTTGTGAGGAGATG	2379
Qy	1240	AGTCTGATGCAACCAAGCGGGGGCCCCGGCTCCAGCCCCCAACCAAGAGAGGG	1299	2398	AGGCTGACAGATGATTCAGTTGAGGAAGTGTGAGTTCGGGGCTTGTGAGGAGATG	2457
Db	1321	AGTCTGATGCAACCAAGCGGGGGCCCCGGCTCCAGCCCCCAACCAAGAGAGGG	1380	2380	GCTTCTGTGCTGGGACCAACCCACATCTGGTTGAGTTGGAACCTGTGACAGAAATGCACGTG	2439
Qy	1300	TTGTGCTCTTGGCGGACAGTGGGCTGTGAAATCAGAAATCCTATTGAGGAGCAGGAC	1359	2458	GCTTCTGTGCTGGGACCAACCCACATCTGGTTGAGTTGGAACCTGTGACAGAAATGCACGTG	2517
Db	1381	TTGTGCTCTTGGCGGACAGTGGGCTGTGAAATCAGAAATCCTATTGAGGAGCAGGAC	1440	2440	GAGGATTTGGGCTGAGGTTACTATGCCAGGACTGAGGACCCAGTCTGCGACATACGG	2499
Qy	1360	CTCCGGAAGCAGCGCTTAGACGGGAGAGCTCTGCTCTGCTTCAACATGAACATCTTC	1419	2518	GAGGATTTGGGCTGAGGTTACTATGCCAGGACTGAGGACCCAGTCTGCGACATACGG	2577
Db	1441	CTCCGGAAGCAGCGCTTAGACGGGAGAGCTCTGCTCTGCTTCAACATGAACATCTTC	1500	2500	ACTTTGTGGCTGAAAGATCTGCCGCTCTCACTGCTGCTGTGACGAGCTGGGCTCAACT	2637
Qy	1420	CAGAAGACATCAACTGTGAGAGTACTACAGCTTTCATCCACTTGTGATTTCCAGGAATTC	1479	2578	ACTTTGTGGCTGAAAGATCTGCCGCTCTCACTGCTGCTGTGACGAGCTGGGCTCAACT	2637
Db	1501	CAGAAGACATCAACTGTGAGAGTACTACAGCTTTCATCCACTTGTGATTTCCAGGAATTC	1560	2560	CTCAGTGTGAAACGAGCCTGAGAGCTGGAACCTGAGCTGATGAGCTGGGGGACCTC	2619
Qy	1480	TTTTCAGCTATGTATATATCTTGAACGAGGGGAGCGGGGACCGCCAGCAGCAGGAC	1539	2638	CTCAGTGTGAAACGAGCCTGAGAGCTGGAACCTGAGCTTGAATGAGCTGGGGGACCTC	2697
Db	1561	TTTTCAGCTATGTATATATCTTGAACGAGGGGAGCGGGGACCGCCAGCAGCAGGAC	1620	2620	GGGGTCTGCTGTGTGTGAGGGCTCAGGACATCCACGTGCAAGCTCCAGACCTTCGCGG	2679
Qy	1540	GTGACAGGCTGTGT				

Db 2758 TTGGGCATCTGCCGCTGGGCTCTGCCGCTGTGAGGCTCTTTCTGTGGTCTCAAGGCC 2817
Qy 2740 AACCAACCTCCGGAGCTGGACTTGAGTTTCAACGACCTGGGAGACTGGGGCTGTGG 2799
Db 2818 AACCAACCTCCGGAGCTGGACTTGAGTTTCAACGACCTGGGAGACTGGGGCTGTGG 2877
Qy 2800 TTGCTGGCTGAGGGCTCAACATCCCGCTTGCAGACTCCAGAACTGTGGCTGGATGC 2859
Db 2878 TTGCTGGCTGAGGGCTCAACATCCCGCTTGCAGACTCCAGAACTGTGGCTGGATGC 2937
Qy 2860 TGTGCTCTCACAGCCCAAGCTTGTGAGATCTTTACTTTCACCTGGGGATCAACGACC 2919
Db 2938 TGTGCTCTCACAGCCCAAGCTTGTGAGATCTTTACTTTCACCTGGGGATCAACGACC 2997
Qy 2920 TTGACCGACCTTACCTGACCAACAAACGCTTAGGGACACAGGTGTCCGACTGCTTGC 2979
Db 2998 TTGACCGACCTTACCTGACCAACAAACGCTTAGGGACACAGGTGTCCGACTGCTTGC 3057
Qy 2980 AAGCGCTGAGCATCTCTGGCTGCAACTCCGAGTCTCTCTGGTATTGATGGAGACTG 3039
Db 3058 AAGCGCTGAGCATCTCTGGCTGCAACTCCGAGTCTCTCTGGTATTGATGGAGACTG 3117
Qy 3040 AATAAATGACCCAGTAGGTGCGAGCGCTTCGAGTAACAAACCTTATTGACATT 3099
Db 3118 AATAAATGACCCAGTAGGTGCGAGCGCTTCGAGTAACAAACCTTATTGACATT 3177
Qy 3100 GGCTGCTGA 3108
Db 3178 GGCTGCTGA 3186

RESULT 6

ADF94754
ID ADF94754 standard; cDNA; 3186 BP.
XX
AC ADF94754;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human PYRIN-8 coding sequence #3.
XX
KW human; PYRIN; inflammatory disorder; inappropriate apoptosis;
KW inflammatory bowel disease; rheumatoid arthritis; diabetes;
KW multiple sclerosis; Grave's disease; contact dermatitis; psoriasis;
KW graft rejection; asthma; allergy; chronic obstructive pulmonary disease;
KW glomerulonephritis; infection; Alzheimer's disease; Parkinson's disease;
KW anaemia; ischaemia; screening; chromosomal mapping; tissue typing;
KW forensic biology; pharmacogenomics; predictive medicine; gene; ss.
XX
OS Homo sapiens.
XX
FN WO2003089588-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-US011572.
XX
PR 17-APR-2002; 2002US-00124498.
XX
PA (MILL-) MILLENNIUM PHARM INC.
FA (AMHP) WYETH.
XX
PI Bertin J, Wang W, Blatcher M;
XX
DR WPI; 2003-845527/78.
DR P-PSDB; ADF94755.
XX
PT New nucleic acid molecules and polypeptides (e.g. PYRIN-2 or PYRIN-3)
PT useful for diagnosing, preventing or treating inflammation or disorders
PT associated with inappropriate apoptosis, in chromosomal mapping or in
PT pharmacogenomics.
XX
PS Claim 4; SEQ ID NO 17; 199pp; English.

XX The invention comprises the amino acid and coding sequences of human
CC PYRIN proteins. The DNA and protein sequences of the invention are useful
CC in diagnosing, preventing and treating inflammatory disorders or
CC disorders associated with inappropriate apoptosis, such as: inflammatory
CC bowel disease, rheumatoid arthritis, diabetes, multiple sclerosis,
CC Grave's disease, contact dermatitis, psoriasis, graft rejection, asthma,
CC allergy, chronic obstructive pulmonary disease, glomerulonephritis,
CC infections, Alzheimer's disease, Parkinson's disease, anaemia and
CC ischaemia. The DNA and protein sequences of the invention may also be
CC used in screening assays, chromosomal mapping, tissue typing, forensic
CC biology, pharmacogenomics, predictive medicine, and in monitoring of
CC clinical trials. The present DNA sequence encodes a PYRIN protein of the
CC invention.
XX

SQ Sequence 3186 BP; 701 A; 908 C; 945 G; 632 T; 0 U; 0 Other;

Query Match 96.5%; Score 2997.8; DB 10; Length 3186;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 3103; Conservative 0; Mismatches 2; Indels 84; Gaps 2;

Qy 1 ATGCTACGAACCCGACGAGCGGCTCTGTGCGCTGTCCACTTACTTGGAGAACTC 60
Db 1 ATGCTACGAACCCGACGAGCGGCTCTGTGCGCTGTCCACTTACTTGGAGAACTC 60
Qy 61 GAGGCTGTGAACTGAAAGATTCAAGTTATACCTGGGGACCGCGACAGAGCTGGAGAA 120
Db 61 GAGGCTGTGAACTGAAAGATTCAAGTTATACCTGGGGACCGCGACAGAGCTGGAGAA 120
Qy 121 GCGAAGATCCCTGGGGAGCATGGAAGAGCGGCTCCCTTGGAAATGGCCAGCTGCTC 180
Db 121 GCGAAGATCCCTGGGGAGCATGGAAGAGCGGCTCCCTTGGAAATGGCCAGCTGCTC 180
Qy 181 ATCACCACATTCGGGCCAGAGGAGGCTGGAGTTGGCTCTCAGCAGCTTTGAGCGGATA 240
Db 181 ATCACCACATTCGGGCCAGAGGAGGCTGGAGTTGGCTCTCAGCAGCTTTGAGCGGATA 240
Qy 241 AACAGGAAGACCTGTGGGAGAGGACAGAGAGGAGGACCTGTGTGAGG----- 288
Db 241 AACAGGAAGACCTGTGGGAGAGGACAGAGAGGAGGACCTGTGTGAGGATACCCACCT 300
Qy 289 ----- 288
Db 301 GGTGGCCGCTCTCACTTGGGAAACAGTCAACATGCCCTCTTGGAAAGTCTCTTGTCACT 360
Qy 289 -----GATCCCGAGGAAACCTACAGGAGCTATGTCCGCGAGGAATTCGCGCTCATG 339
Db 361 CCAAGAAAGATCCCGAGGAAACCTACAGGAGCTATGTCCGCGAGGAATTCGCGCTCATG 420
Qy 340 GAAGACCGCAATGCGGCTTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC 399
Db 421 GNAGCCGCAATGCGGCTTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC 480
Qy 400 CTGCTGTGAAAGAGCACTCAAAACCCCATGCGAGTCCAGCAGCAGCTTTGGACACAGGC 459
Db 481 CTGCTGTGAAAGAGCACTCAAAACCCCATGCGAGTCCAGCAGCAGCTTTGGACACAGGC 540
Qy 460 CCGGGACACCGGAGGACCGTGGGACACCGAGCTAGCCCATCAAGTAGAGACCTCTTT 519
Db 541 CCGGGACACCGGAGGACCGTGGGACACCGAGCTAGCCCATCAAGTAGAGACCTCTTT 600
Qy 520 GAGCCAGACGAGGAGGCGCCCGGAGCCACCGCGACCGTGTGTATGCAAGCGCGGACGG 579
Db 601 GAGCCAGACGAGGAGGCGCCCGGAGCCACCGCGACCGTGTGTATGCAAGCGCGGACGG 660
Qy 580 ATAGGCAAGTCCATGTGGCACAAGAGTGTGACTGTGGCTGGCGCGAGAGCTTCTTC 639
Db 661 ATAGGCAAGTCCATGTGGCACAAGAGTGTGACTGTGGCTGGCGCGAGAGCTTCTTC 720
Qy 640 CAAGGAGATTTGATTTATCTTCTACATCAACTGCGAGGAGATGACACAGAGTGCCACG 699
Db 721 CAAGGAGATTTGATTTATCTTCTACATCAACTGCGAGGAGATGACACAGAGTGCCACG 780

QY 700 GAATGAGGATGCAAGACCTCATCTTCAGTGTCTGGCTGAGCCAGCGCGCTCTCCAG 759
Db 781 GAATGAGCATGCAAGACCTCATCTTCAGTGTCTGGCTGAGCCAGCGCGCTCTCCAG 840
QY 760 GAGTCATCCGAGTCTCCGAGCGCTCTCTTCATCATCGACGGCTTCGATGAGTCAAG 819
Db 841 GAGTCATCCGAGTCTCCGAGCGCTCTCTTCATCATCGACGGCTTCGATGAGTCAAG 900
QY 820 CCTTTCTTCCAGATCTCTCAGGACCTCGTGGTCTCTGTGGAGAGAGAAAGCGCCACG 879
Db 901 CCTTTCTTCCAGATCTCTCAGGACCTCGTGGTCTCTGTGGAGAGAGAAAGCGCCACG 960
QY 880 GAGTCGTCTTAAACAGCTTAAATTCGGAAGAGCTCTCCCTGAGCTATCTTTGCTCATC 939
Db 961 GAGTCGTCTTAAACAGCTTAAATTCGGAAGAGCTCTCCCTGAGCTATCTTTGCTCATC 1020
QY 940 ACCACAGCGCCACGGCTTTGGAGAGCTCCACCGTCTGTGGAGCACCCAGGCAATGTG 999
Db 1021 ACCACAGCGCCACGGCTTTGGAGAGCTCCACCGTCTGTGGAGCACCCAGGCAATGTG 1080
QY 1000 GAGATCTGGGCTTCTCTGAGGCGAAGAAAGAAATACCTCTCAAGTATTTCCACAAT 1059
Db 1081 GAGATCTGGGCTTCTCTGAGGCGAAGAAAGAAATACCTCTCAAGTATTTCCACAAT 1140
QY 1060 GCAGAGCAGCGCGCCAGTCTTCAATTTAGTGAGGACAAACGAGCTCTCTTCAACATG 1119
Db 1141 GCAGAGCAGCGCGCGCAAGTCTTCAATTTAGTGAGGACAAACGAGCTCTCTTCAACATG 1200
QY 1120 TGTCTGTCTCCCTGTGTGTGTGGTGTGTGTGTAACCTGCTCCAGCAGCAGCTGGAGGT 1179
Db 1201 TGTCTGTCTCCCTGT 1260
QY 1180 GGGGGCTGTGTGAGACAGCTCAGAGCACCACTGAGTGTATCTCTACCTGCTG 1239
Db 1261 GGGGGCTGTGTGAGACAGCTCAGAGCACCACTGAGTGTATCTCTACCTGCTG 1320
QY 1240 AGTCTGATGCAACCAAGCGGGGGCCCGCGCTCCAGCGCCCAACCAACAGAGAGG 1299
Db 1321 AGTCTGATGCAACCAAGCGGGGGCCCGCGCTCCAGCGCCCAACCAACAGAGAGG 1380
QY 1300 TTGTGCTCTCTTGGCGCAGATGGGCTCTGGAAATCAGAAATCTTATTTGAGGAGGAG 1359
Db 1381 TTGTGCTCTCTTGGCGCAGATGGGCTCTGGAAATCAGAAATCTTATTTGAGGAGGAG 1440
QY 1360 CTCGGAGACAGCGCTAGACGGGAGACCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1419
Db 1441 CTCGGAGACAGCGCTAGACGGGAGACCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1500
QY 1420 CAGAAGGACATCAACTGTGAGAGTACTACAGCTTCACTTCACTTGAATTTCCAGGAATC 1479
Db 1501 CAGAAGGACATCAACTGTGAGAGTACTACAGCTTCACTTCACTTGAATTTCCAGGAATC 1560
QY 1480 TTTGAGCTATGTATATATCTGACAGGGGGGCGGGGAGGCGGCGGCGGCGGCGGCGGCG 1539
Db 1561 TTTGAGCTATGTATATATCTGACAGGGGGGAGGCGGCGGCGGCGGCGGCGGCGGCGG 1620
QY 1540 GTGACAGCGCTCTGACCGAGTACCGCTTTCTGAAAGAGCTTCTCTGCACTCACAGC 1599
Db 1621 GTGACAGCGCTCTGACCGAGTACCGCTTTCTGAAAGAGCTTCTCTGCACTCACAGC 1680
QY 1600 CGCTTCTCTTTTGGACTCTCTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1659
Db 1681 CGCTTCTCTTTTGGACTCTCTGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740
QY 1660 TGAAGGTCTCGCGGACATCAAGATGACCTGTGTGAGTGTGATCCAAAGCAAGCTCAG 1719
Db 1741 TGAAGGTCTCGCGGACATCAAGATGACCTGTGTGAGTGTGATCCAAAGCAAGCTCAG 1800
QY 1720 AGCGAGGCTCCACCTCTGAGCAGGAGGCTCTTTGGAGTCTCTTCACTGCTGTGTGAGATC 1779
Db 1801 AGCGAGGCTCCACCTCTGAGCAGGAGGCTCTTTGGAGTCTCTTCACTGCTGTGTGAGATC 1860
QY 1780 CAGGAGGAGGAGTGTATTCAGCAGGCGGCTGAGGCGCTTCCAGGTGATCGTGTGAGCAAC 1839

Db 1861 CAGGAGGAGGAGTGTATTCAGCAGGCGGCTGAGGCGCTTCCAGGTGATCGTGTGAGCAAC 1920
QY 1840 ATTGCTCTCAAGATGAGGACATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1899
Db 1921 ATTGCTCTCAAGATGAGGACATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
QY 1900 CAGGTGTGTGACTTGTATGCGCCACCTTACAGCGCGGAGCGGGGAGAGCCGCGGAGGTGC 1959
Db 1981 CAGGTGTGTGACTTGTATGCGCCACCTTACAGCGCGGAGCGGGGAGAGCCGCGGAGGTGC 2040
QY 1960 TCCGAGGAGCGCACACGCTCTGTGTGAGCTCAGACGAGAGAGACCGTCTCTCTCTCTCT 2019
Db 2041 TCCGAGGAGCGCACACGCTCTGTGTGAGCT---ACCAGAGAGGACCGTCTCTCTCTCTCT 2097
QY 2020 GCCTACAGTGAACATCTGCGCAGCGCGCTGTGCAACCAATCCAAACCTCTGATAGAGTGTCT 2079
Db 2098 GCCTACAGTGAACATCTGCGCAGCGCGCTGTGCAACCAATCCAAACCTCTGATAGAGTGTCT 2157
QY 2080 CTGTACCGAAATGCGCTGCGCAGCGCGGGGTGAAGCTGTCTGTCAAGGATCTCAGACAC 2139
Db 2158 CTGTACCGAAATGCGCTGCGCAGCGCGGGGTGAAGCTGTCTGTCAAGGATCTCAGACAC 2217
QY 2140 CCCAACTGCAAACTTTCAGAACTTGAAGCTGTGAAGGTGCGCATCTCCAGCTCAGCCTGC 2199
Db 2218 CCCAACTGCAAACTTTCAGAACTTGAAGCTGTGAAGGTGCGCATCTCCAGCTCAGCCTGC 2277
QY 2200 GAGGACCTCTCTGCACTCTCATAGCCAAATTAAGAAATTTGACAAAGATGATCTCAGTGGC 2259
Db 2278 GAGGACCTCTCTGCACTCTCATAGCCAAATTAAGAAATTTGACAAAGATGATCTCAGTGGC 2337
QY 2260 AACGGCTTGGATTTCCAGGCAATGATCTGTCTTCCGAGGGCTTCCGCGCATCTCCAGTGC 2319
Db 2338 AACGGCTTGGATTTCCAGGCAATGATCTGTCTTCCGAGGGCTTCCGCGCATCTCCAGTGC 2397
QY 2320 AGCTGTCAGATCAATTCAGTTGAGGAGTGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2379
Db 2398 AGCTGTCAGATCAATTCAGTTGAGGAGTGTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2457
QY 2380 GCTTCTGTCTCTGCGCACCAACCCACATCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2439
Db 2458 GCTTCTGTCTTGGCACCAACCCACATCTGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 2517
QY 2440 GAGGATTTGGCTGAGGTTACTATGCGAGGACCTGAGGCGACCCAGTCTGAGAGCTACGG 2499
Db 2518 GAGGATTTGGCTGAGGTTACTATGCGAGGACCTGAGGCGACCCAGTCTGAGAGCTACGG 2577
QY 2500 ACTTTGTGCTGAAGATCTGCGCGCTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2559
Db 2578 ACTTTGTGCTGAAGATCTGCGCGCTCACTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2637
QY 2560 CTGAGTGTGAACAGAGCTGAGAGCTGGACCTGAGGCTGAAATGAGCTGGGGGACCTC 2619
Db 2638 CTGAGTGTGAACAGAGCTGAGAGCTGGACCTGAGGCTGAAATGAGCTGGGGGACCTC 2697
QY 2620 GGGGTGCTGTCTGTGAGGCGCTCAGGCAATCCACGTCGAACTCCAGACCTCTGCGG 2679
Db 2698 GGGGTGCTGTCTGTGAGGCGCTCAGGCAATCCACGTCGAACTCCAGACCTCTGCGG 2757
QY 2680 TTGGGATCTGCGGCTGGGCTCTGCGCGCTGTGAGGGTCTTTCTGTGTGTCTCTCAGGCG 2739
Db 2758 TTGGGATCTGCGGCTGGGCTCTGCGCGCTGTGAGGGTCTTTCTGTGTGTCTCTCAGGCG 2817
QY 2740 AACCAACCTCTCGGAGCTGGAATTGAGTTTCAAAGCTGGGAGACTGGGGGCTGTGG 2799
Db 2818 AACCAACCTCTCGGAGCTGGAATTGAGTTTCAAAGCTGGGAGACTGGGGGCTGTGG 2877
QY 2800 TTGCTGCTCAGGGGCTGCAACATCCCGCTGAGACTCCAGAAATCTGTGGCTTGGATAGC 2859
Db 2878 TTGCTGCTCAGGGGCTGCAACATCCCGCTGAGACTCCAGAAATCTGTGGCTTGGATAGC 2937
QY 2860 TGTGGCTCAGCAGAGGCTTGTGAAATCTTTTATCTTCACTCTGGGATCAACAGGAC 2919

Ds	2938	TGTGGCTCAGAGCAAGGCTTGTGAGAACTTTTACCTTCCCTGGGGATCAACAGACC	2997
Qy	2920	TTGACCGACCTTTACCTGACCAACAGCCCTAGGGGACACAGGTGTCCGACTGCTTTGC	2979
Ds	2998	TTGACCGACCTTTACCTGACCAACAGCCCTAGGGGACACAGGTGTCCGACTGCTTTGC	3057
Qy	2980	AAGGGCTGAGCATCTCGGCTGCAAACTCCGAGTCTCTGGTTATTTGGGATGGACCTG	3039
Ds	3058	AAGGGCTGAGCATCTCGGCTGCAAACTCCGAGTCTCTGGTTATTTGGGATGGACCTG	3117
Qy	3040	AATAAATGACCCACAGTAGCTTGGCAGCGCTTCGAGTAAACAAACCTTATTTGGACATT	3099
Ds	3118	AATAAATGACCCACAGTAGCTTGGCAGCGCTTCGAGTAAACAAACCTTATTTGGACATT	3177
Qy	3100	GGCTGCTGA 3108	
Ds	3178	GGCTGCTGA 3186	
RESULT 7			
ID	ADJ19382		
XX	ADJ19382 standard; cDNA; 3218 BP.		
AC	ADJ19382;		
DT	20-MAY-2004 (first entry)		
XX	Human PAN6 PAAD domain-containing protein full-length cDNA 2.		
DE			
XX	PAAD; cytostatic; cancer; gene therapy; human; PAAD domain; ss; gene;		
KW	PAN6.		
KW			
OS	Homo sapiens.		
XX			
XX	US2004002593-A1.		
PN			
PD	01-JAN-2004.		
XX			
XX	04-APR-2003; 2003US-00407866.		
XX			
PR	04-APR-2002; 2002US-0370538P.		
XX			
FA	(REED/) REED J C.		
PA	(GODZ/) GODZIK A.		
XX			
PI	Reed JC, Godzik A;		
XX			
DR	WPI; 2004-061677/06.		
DR	P-PSDB; ADJ19383.		
XX			
PT	New nucleic acid molecule encoding a PAAD-containing polypeptide, useful		
PT	for preparing a composition for diagnosing or treating e.g., cancer.		
XX			
PS	Disclosure; SEQ ID NO 67; 193pp; English.		
XX			
CC	The invention relates to a novel isolated nucleic acid molecule encoding		
CC	a PAAD-containing polypeptide. The polypeptide of the invention		
CC	demonstrates cytostatic activity and may be useful for preparing a		
CC	composition for diagnosing or treating diseases associated with the PAAD		
CC	domain-containing polypeptide, such as cancer, via gene therapy. The		
CC	current sequence is that of the human PAAD domain-containing protein full		
CC	-length cDNA of the invention.		
XX			
SQ	Sequence 3218 BP; 691 A; 935 C; 958 G; 634 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 94.2%; Score 2929; DB 12; Length 3218;			
Matches 3020; Conservative 0; Mismatches 0; Indels 81; Gaps 1;			
Qy	1	ATGCTACGAACCGCAGGACGCGCTCTGTGCGCTGTCCACCTACTTGGAGAATCTC	60
Ds	118	ATGCTACGAACCGCAGGACGCGCTCTGTGCGCTGTCCACCTACTTGGAGAATCTC	177

Qy	61	GAGCTGTGAACTGAAGAAAGTTCAAGTTATACCTGGGACCGCGACAGAGCTGGGAGAA	120
Ds	178	GAGCTGTGAACTGAAGAAAGTTCAAGTTATACCTGGGACCGCGACAGAGCTGGGAGAA	237
Qy	121	GGCAAGATCCCTGGGGAAGCATGGAGAGCGGCTCCCTGGAAATGGCCAGCTGCTC	180
Ds	238	GGCAAGATCCCTGGGGAAGCATGGAGAGCGGCTCCCTGGAAATGGCCAGCTGCTC	297
Qy	181	ATCACCCACATTCGGGCGCAGAGAGGCTGTGAGGTGGCTCTCAGCACCTTTGAGCGGATA	240
Ds	298	ATCACCCACATTCGGGCGCAGAGAGGCTGTGAGGTGGCTCTCAGCACCTTTGAGCGGATA	357
Qy	241	AACAGGAAGACCTGTGGGAGAGGACACAGAGAGGACCTGTGTGAGG-----	288
Ds	358	AACAGGAAGACCTGTGGGAGAGGACACAGAGAGGACCTGTGTGAGGATACCCACCT	417
Qy	289	-----	288
Ds	418	GGTGGCCGCTCTCACTTGGGAACCAAGTCAACATGCGCTTCTGGAAGTCTCTTTGTCACT	477
Qy	289	-----GATCCCGCAGGAAACCTACAGGAGACTATGTCCGCGAGGAAATTCGGCTCATG	339
Ds	478	CCAAGAAAGATCCCGCAGGAAACCTACAGGAGACTATGTCCGCGAGGAAATTCGGCTCATG	537
Qy	340	GAAGACCGCAATGCGCGCTTAGGGGAATGTCAACCTCAGCCACCGGTACACCCGGCTC	399
Ds	538	GAAGACCGCAATGCGCGCTTAGGGGAATGTCAACCTCAGCCACCGGTACACCCGGCTC	597
Qy	400	CTGCTGTGAGGAGCACTCAAAACCCCATGAGGTCCAGGAGGAGCTTCTGGACACAGGC	459
Ds	598	CTGCTGTGAGGAGCACTCAAAACCCCATGAGGTCCAGGAGGAGCTTCTGGACACAGGC	657
Qy	460	CGGGGACACGCGAGGACCGGTGGGACACCAAGCTAGCCCATCAAGATAGAGACCTCTTT	519
Ds	658	CGGGGACACGCGAGGACCGGTGGGACACCAAGCTAGCCCATCAAGATAGAGACCTCTTT	717
Qy	520	GAGCCAGACGAGGAGCGCCCGGACCAACCGGCAACCGTGTCTATGCAAGGCGCGCAGGG	579
Ds	718	GAGCCAGACGAGGAGCGCCCGGACCAACCGGCAACCGTGTCTATGCAAGGCGCGCAGGG	777
Qy	580	ATAGGCAAGTCCATGCTGGCACACAGGTGATGCTGGACTGGGCGGACGGAGCTCTTC	639
Ds	778	ATAGGCAAGTCCATGCTGGCACACAGGTGATGCTGGACTGGGCGGACGGAGCTCTTC	837
Qy	640	CAAGGCAGATTTGATTTATCTTCTACATCAACTGACGAGGAGATGAACAGAGTGCCACG	699
Ds	838	CAAGGCAGATTTGATTTATCTTCTACATCAACTGACGAGGAGATGAACAGAGTGCCACG	897
Qy	700	GAATGACAGATCAAGACCTCATCTTCAGCTGTGGCTGTGAGCCAGCGGCGCTCTCCAG	759
Ds	898	GAATGACAGATCAAGACCTCATCTTCAGCTGTGGCTGTGAGCCAGCGGCGCTCTCCAG	957
Qy	760	GAGCTCATCGAGTTCCCGAGCGCTCTTTTATCATCATCGAGCTTCGATGAGCTCAAG	819
Ds	958	GAGCTCATCGAGTTCCCGAGCGCTCTTTTATCATCATCGAGCTTCGATGAGCTCAAG	1017
Qy	820	CTTCTTTTCCACGATCTCAGGAGACCTGTGTGCTCTGTCTGGGAGGAGAAACGCCACG	879
Ds	1018	CTTCTTTTCCACGATCTCAGGAGACCTGTGTGCTCTGTCTGGGAGGAGAAACGCCACG	1077
Qy	880	GAGCTGCTTTTAAACAGCTTAAATCGGAAGAGTGTCTCCCTGAGCTATCTTTGCTCATC	939
Ds	1078	GAGCTGCTTTTAAACAGCTTAAATCGGAAGAGTGTCTCCCTGAGCTATCTTTGCTCATC	1137
Qy	940	ACCACAGGCGCCAGGCTTTGGAGAGCTCCACGCTGTCTGGAGCACCCAGGCATGTG	999
Ds	1138	ACCACAGGCGCCAGGCTTTGGAGAGCTCCACGCTGTCTGGAGCACCCAGGCATGTG	1197
Qy	1000	GAGATCTGGGCTTCTCTGAGGAGAGAAAGGAATACTTCTACAGTATTTCCACAAT	1059
Ds	1198	GAGATCTGGGCTTCTCTGAGGAGAGAAAGGAATACTTCTACAGTATTTCCACAAT	1257
Qy	1060	GCAGAGCAGCGGGCCAAAGTCTTCAATTACGTGAGGAGCAACGAGGCCTCTCTTCCACCATG	1119

KW inflammatory disease; cancer; gene therapy; human; gene; ss; purine;
KW CATERPILLER 19.3; chromosome 19q13; multiple sclerosis; isoform II.
XX
OS Homo sapiens.
XX
XX WO2004034093-A2.
XX
XX 22-APR-2004.
PD
XX
XX 30-APR-2003; 2003WO-US013562.
PF
XX
XX 30-APR-2002; 2002US-0376626P.
PR
XX
XX (UTNC-) UNIV NORTH CAROLINA.
PA
XX
XX Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'Connor W;
PI Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;
XX
XX WPI; 2004-348215/32.
DR
XX P-PSDB; ADP47726.
XX
XX
XX New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3,
PT CATERPILLAR 16.1, CATERPILLER 16.2 or CIAS1 polypeptide, useful in
PT preparing a composition for treating inflammatory disease or cancer.
XX
XX Claim 4; SEQ ID NO 3; 205pp; English.
XX
XX The invention relates to a novel isolated nucleic acid encoding a Monarch
CC -1, CATERPILLER (CARD [caspase recruitment domain], transcription
CC enhancer, [R(purine)-binding, pyrin, lots of leucine repeats] 11.2,
CC CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 (cold-
CC induced autoinflammatory syndrome 1) polypeptide comprising the amino
CC acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or
CC its fragment. The nucleic acid of the invention demonstrates
CC antiinflammatory and cytostatic activities and may be useful in preparing
CC a composition for treating an inflammatory disease or cancer, possibly
CC via gene therapy. The current sequence is that of the human Monarch-1
CC (CATERPILLER 19.3) isoform II cDNA of the invention which is located on
CC chromosome 19q13, in the multiple sclerosis susceptibility region.
XX
XX Sequence 3563 BP; 805 A; 992 C; 1050 G; 716 T; 0 U; 0 Other;
SQ

Query Match 88.8%; Score 2759; DB 12; Length 3563;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2850; Conservative 0; Mismatches 0; Indels 81; Gaps 1;
1 ATGCTACGAAACCGCAGGAGGAGCGCTCTGTGCGCTGTCCACTACTTGGAGAACTC 60
221 ATGCTACGAAACCGCAGGAGGAGCGCTCTGTGCGCTGTCCACTACTTGGAGAACTC 280
61 GAGGCTGTGGAACTGAAGAAGTTCAAGTTATACCTGGGGACCGGACAGAGCTGGGAGAA 120
281 GAGGCTGTGGAACTGAAGAAGTTCAAGTTATACCTGGGGACCGGACAGAGCTGGGAGAA 340
121 GGCAAGATCCCTCGGGAGCATGGAGAGCCGGTCCCTCGGAAATGGCCACGCTGCTC 180
341 GGCAAGATCCCTCGGGAGCATGGAGAGCCGGTCCCTCGGAAATGGCCACGCTGCTC 400
181 ATACCCACTTCGGGCCAGAGAGGCGCTGGAGGTGGCTCTCAGCACCTTTGAGCGGATA 240
401 ATACCCACTTCGGGCCAGAGAGGCGCTGGAGGTGGCTCTCAGCACCTTTGAGCGGATA 460
241 AACAGGAGGACCTGTGGGAGAGGAGGACAGAGAGGAGGACCTGGTGAGG----- 288
461 AACAGGAGGACCTGTGGGAGAGGAGGACAGAGAGGAGGACCTGGTGAGGATACCCACCT 520
289 ----- 288
521 GGTGGCCGTCCTCACTTGGGAACCAAGTCAACATGCGCTTCTGGAAGTCTCTCTTGTCACT 580
289 -----GATCCCCAGGAAACCTACAGGAGCTATGTCCGACGAGAAATTCGCGCTCATG 339
581 CCAAGAAAAGATCCCCAGGAAACCTACAGGAGCTATGTCCGACGAGAAATTCGCGCTCATG 640

Qy 340 GAAGACCGCAATGCGCGCTTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC 399
Db 641 GAAGACCGCAATGCGCGCTTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC 700
Qy 400 CTGCTGGTGAAGGAGCACTCAAAACCCCATGCAAGTCCAGGAGCACTTCTGGACACAGGC 459
Db 701 CTGCTGGTGAAGGAGCACTCAAAACCCCATGCAAGTCCAGGAGCACTTCTGGACACAGGC 760
Qy 460 CGGGGACACCGGAGGACCGTGGGACACACCGGCTAGCCCATCAAGATAGAGACCTCTTT 519
Db 761 CGGGGACACCGGAGGACCGTGGGACACACCGGCTAGCCCATCAAGATAGAGACCTCTTT 820
Qy 520 GAGCCAGACGAGGAGCGCCCCGAGCCACCGCCACCGTGTGTCTATGCAAGCGCGGACAGG 579
Db 821 GAGCCAGACGAGGAGCGCCCCGAGCCACCGCCACCGTGTGTCTATGCAAGCGCGGACAGG 880
Qy 580 ATAGGCAAGTCCATGCTGGGACACACAGGTCATGCTGGGAGCGGAGAGCTTCTTC 639
Db 881 ATAGGCAAGTCCATGCTGGGACACACAGGTCATGCTGGGAGCGGAGAGCTTCTTC 940
Qy 640 CAAGGCAAGTTCGATTATCTTCTCATCACTGAGGAGATGAACACGAGTGCCACG 699
Db 941 CAAGGCAAGTTCGATTATCTTCTCATCACTGAGGAGATGAACACGAGTGCCACG 1000
Qy 700 GAATGCAAGCATGCAAGACCTCATCTTTCAGCTGTGGCTGAGCCGACGCGCTTCTCCAG 759
Db 1001 GAATGCAAGCATGCAAGACCTCATCTTTCAGCTGTGGCTGAGCCGACGCGCTTCTCCAG 1060
Qy 760 GAGCTCATCGAGTCCGAGCGCTCTTTTCATCATCGACGGCTTCGATGAGTCAAG 819
Db 1061 GAGCTCATCGAGTCCGAGCGCTCTTTTCATCATCGACGGCTTCGATGAGTCAAG 1120
Qy 820 CCTTCTTTCACGATCCTCAGGAGACCTGTGTCTGTGGGAGGAGAAACGSCCCACG 879
Db 1121 CCTTCTTTCACGATCCTCAGGAGACCTGTGTCTGTGGGAGGAGAAACGSCCCACG 1180
Qy 880 GAGCTGTCTTAAACAGCTTAAATTCGGAAGAAGTGTCTCCTGAGCTATCTTTGCTCATC 939
Db 1181 GAGCTGTCTTAAACAGCTTAAATTCGGAAGAAGTGTCTCCTGAGCTATCTTTGCTCATC 1240
Qy 940 ACCACAGCGGCCACGGCTTTGGAGAGCTCCAGCTGTCTGTGGAGCACCCGAGCATGTG 999
Db 1241 ACCACAGCGGCCACGGCTTTGGAGAGCTCCAGCTGTCTGTGGAGCACCCGAGCATGTG 1300
Qy 1000 GAGATCCTGGCTTCTCTGAGGAGGAGAAAGAAATACCTTCTACAAAGTATTTCCACAAT 1059
Db 1301 GAGATCCTGGCTTCTCTGAGGAGGAGAAAGAAATACCTTCTACAAAGTATTTCCACAAT 1360
Qy 1060 GCAGAGCAGCGCGGCCCAAGTCTTCAATTACGTGAGGAGCAACGAGCCTCTCTTCAACCATG 1119
Db 1361 GCAGAGCAGCGCGGCCCAAGTCTTCAATTACGTGAGGAGCAACGAGCCTCTCTTCAACCATG 1420
Qy 1120 TGCTTGTCTCCCTGT 1179
Db 1421 TGCTTGTCTCCCTGT 1480
Qy 1180 GGGGGGCTGTGAGACAGAGCTCCAGGACCAACCACTGCAAGTGTACATGTCTTACCTGTG 1239
Db 1481 GGGGGGCTGTGTGAGACAGAGCTCCAGGACCAACCACTGCAAGTGTACATGTCTTACCTGTG 1540
Qy 1240 AGTCTGATGCAACCCCAAGCGGGGGCCCCCGCGCTCCAGCGCCCCCACCACCAACGAGAGGG 1299
Db 1541 AGTCTGATGCAACCCCAAGCGGGGGCCCCCGCGCTCCAGCGCCCCCACCACCAACGAGAGGG 1600
Qy 1300 TTGTGTCTCTTGGCGGAGATGGGCTCTGGAATCAGAAAAATCTTATTTGAGGAGCAGAC 1359
Db 1601 TTGTGTCTCTTGGCGGAGATGGGCTCTGGAATCAGAAAAATCTTATTTGAGGAGCAGAC 1660
Qy 1360 CTCGGAGACACCGCTTAGCGGGAGAGCTCTTGCCTTCTTCAACATGAACATCTTC 1419
Db 1661 CTCGGAGACACCGCTTAGCGGGAGAGAGCTCTTGCCTTCTTCAACATGAACATCTTC 1720

QY	1420	CAGAAGGACATCAACTGTGAGAGGTACTACAGCTTCATCCACTTGAGTTTCCAGGAATTC	1479
DB	1721	CAGAAGGACATCAACTGTGAGAGGTACTACAGCTTCATCCACTTGAGTTTCCAGGAATTC	1780
QY	1480	TTTGTGAGCTATGTACTATATCTGTGACGAGGGGAGGGCGGGCAGGCCACAGACACGAGAC	1539
DB	1781	TTTGTGAGCTATGTACTATATCTGTGACGAGGGGAGGGCGGGCAGGCCACAGACACGAGAC	1840
QY	1540	GTGACCAAGGCTGTGTGACCGAGTACGCGTTTCTGAAAGAGAGCTTCTCTGGCACTCACACAGC	1599
DB	1841	GTGACCAAGGCTGTGTGACCGAGTACGCGTTTCTGAAAGAGAGCTTCTCTGGCACTCACACAGC	1900
QY	1600	CGCTTCTGTTTGGACTCTGTAACAGGAGAGACAGGAGCCACTCTGGAGAAAGAGTCTCTGCG	1659
DB	1901	CGCTTCTGTTTGGACTCTGTAACAGGAGAGACAGGAGCCACTCTGGAGAAAGAGTCTCTGCG	1960
QY	1660	TGGAAGTGCTCGCGGCACATCAAGATGAGACCTGTTGTCAGTGGATCCAAAGCAAAGCTCAG	1719
DB	1961	TGGAAGTGCTCGCGGCACATCAAGATGAGACCTGTTGTCAGTGGATCCAAAGCAAAGCTCAG	2020
QY	1720	AGCGACGGCTCCACCTGTGACGAGGGCTCTGTGGAGTTCCTTTCAGCTGCTTGTACAGATC	1779
DB	2021	AGCGACGGCTCCACCTGTGACGAGGGCTCTGTGGAGTTCCTTTCAGCTGCTTGTACAGATC	2080
QY	1780	CAGGACGAGAGTTCATCCAGCAGCGCCCTGAGCCACTTCAGAGTGATCGTGTTCAGCAAC	1839
DB	2081	CAGGACGAGAGTTCATCCAGCAGCGCCCTGAGCCACTTCAGAGTGATCGTGTTCAGCAAC	2140
QY	1840	ATTGCTCCCAAGATGGAGCACATGGTCTCTCTGTTCTGTAAGCGCTGCAGGAGCGCC	1899
DB	2141	ATTGCTCCCAAGATGGAGCACATGGTCTCTCTGTTCTGTAAGCGCTGCAGGAGCGCC	2200
QY	1900	CAGGTGCTGCACCTTGATGCGCCACCTACAGCGCGGACGCGGAGAACCGCGCGAGGTGC	1959
DB	2201	CAGGTGCTGCACCTTGATGCGCCACCTACAGCGCGGACGCGGAGAACCGCGCGAGGTGC	2260
QY	1960	TCCGACGAGCGCACACGCTGTTGGTGACCTCAGACCAGAGAGGACCGTTCCTGCTGGAC	2019
DB	2261	TCCGACGAGCGCACACGCTGTTGGTGACCTCAGACCAGAGAGGACCGTTCCTGCTGGAC	2320
QY	2020	GCCTACAGTGAACATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGTATAGAGCTGTCT	2079
DB	2321	GCCTACAGTGAACATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGTATAGAGCTGTCT	2380
QY	2080	CTGTACCAGAAATGCCCTGGGCAGCGCGGGGTGAAGCTGCTCTGTCAAGGACTCAGACAC	2139
DB	2381	CTGTACCAGAAATGCCCTGGGCAGCGCGGGGTGAAGCTGCTCTGTCAAGGACTCAGACAC	2440
QY	2140	CCCAACTGCGAAACTTCAGAACTGAGGCTGAAGAGGTGCGGCATCTCCAGCTCAGGCTGC	2199
DB	2441	CCCAACTGCGAAACTTCAGAACTGAGGCTGAAGAGGTGCGGCATCTCCAGCTCAGGCTGC	2500
QY	2200	GAGGACCTCTCTGCAGCTCTCATAGCCAAATAAGAAATTTGACAAGGATGGAATCTCAGTGGC	2259
DB	2501	GAGGACCTCTCTGCAGCTCTCATAGCCAAATAAGAAATTTGACAAGGATGGAATCTCAGTGGC	2560
QY	2260	AACGGCGTTGGATTCACGAGCATGCTGCTTTGCGAGGGCTCGCGGCATCCCCAGTGC	2319
DB	2561	AACGGCGTTGGATTCACGAGGCATGATGCTGCTTTGCGAGGGCTCGCGGCATCCCCAGTGC	2620
QY	2320	AGGCTGCAGATGATTCAGTTGAGGAAAGTGTGAGCTGGAGTTCGCGGGCTTGTTCAGGAGATG	2379
DB	2621	AGGCTGCAGATGATTCAGTTGAGGAAAGTGTGAGCTGGAGTTCGCGGGCTTGTTCAGGAGATG	2680
QY	2380	GCCTTCGTGCTCGGCACCAACCCACATCTGGTTGAGTTGGAACCTGACAGGAAATGCACTG	2439
DB	2681	GCCTTCGTGCTCGGCACCAACCCACATCTGGTTGAGTTGGAACCTGACAGGAAATGCACTG	2740
QY	2440	GAGGATTTGGGCTGAGGTTACTATGTCACAGGACCTGAGGCACCCAGTCTGCAGACTACGG	2499
DB	2741	GAGGATTTGGGCTGAGGTTACTATGTCACAGGACCTGAGGCACCCAGTCTGCAGACTACGG	2800
QY	2500	ACTTTGTGGCTGAAGATCTGCGGCCCTCACTGCTGCTGCTGTGACAGACTGGCCTCAACT	2559

Db	2801	ACTTTGTGGCTGAAGATCTGCGGCTCACTGCTGCTGCTGTACGAGCTGGGCTCAACT	2861
Qy	2560	CTCAGTGTGAAACAGAGCCTTGAGAGAGCTGGACCTGAGCCTGAATGAGCTGGGGGACCTC	2619
Db	2861	CTCAGTGTGAACAGAGCCTTGAGAGAGCTGGACCTGAGCCTGAATGAGCTGGGGGACCTC	2920
Qy	2620	GGGGTGTGCTGCTGTGTGTGAGGGGCTCAGGCATCCCACTGCAAGCTCCAGACCTTCGGG	2679
Db	2921	GGGGTGTGCTGCTGTGTGTGAGGGCTCAGGCATCCCACTGCAAGCTCCAGACCTTCGGG	2980
Qy	2680	TTGGGCATTCGCGGCTGGGCTTCGCGCTGTGAGGCTCTTTCTGTGTGTGCTCCAGGCC	2739
Db	2981	TTGGGCATTCGCGGCTGGGCTTCGCGCTGTGAGGCTCTTTCTGTGTGTGCTCCAGGCC	3040
Qy	2740	AACCAACCTTCGGGAGCTGGACTTGAGTTTCAACGACCTGGGAGACTGGGGCTGTGG	2799
Db	3041	AACCAACCTTCGGGAGCTGGACTTGAGTTTCAACGACCTGGGAGACTGGGGCTGTGG	3100
Qy	2800	TTGCTGGCTGAGGGGCTGCAACATCCCGCTGCGAGACTCCAGAACTGTGG	2850
Db	3101	TTGCTGGCTGAGGGGCTGCAACATCCCGCTGCGAGACTCCAGAACTGTGG	3151
RESULT 9			
ADMO2033			
ID	ADMO2033 standard; cDNA; 3466 BP.		
XX	ADMO2033;		
AC			
XX	20-MAY-2004 (first entry)		
DT			
DE	Human cDNA of the invention SEQ ID NO:718.		
XX	ss; gene; human; gene therapy; diagnostic marker; pharmaceutical.		
KW			
XX	Homo sapiens.		
OS			
XX	EP1347046-A1.		
PN			
XX	24-SEP-2003.		
PD			
XX	12-APR-2002; 2002EP-00008400.		
PP			
XX	22-MAR-2002; 2002JP-00137785.		
PR			
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.		
PA			
XX	Isozaki T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;		
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;		
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;		
PI	WPI; 2003-723558/69.		
DR	P-PSDB; ADM04476.		
DR			
XX	New polynucleotides and polypeptides are useful in gene therapy, for		
PT	developing a diagnostic marker or medicines for regulating their		
PT	expression and activity, or as a target of gene therapy.		
XX			
XX	Claim 1; SEQ ID NO 718; 305pp; English.		
PS			
XX	The invention relates to a novel human polynucleotide and the encoded		
CC	polypeptide. A polynucleotide of the invention may have a use in gene		
CC	therapy. An oligonucleotide of the invention ADM06773 is useful		
CC	as a primer for synthesizing the polynucleotide or as a probe for		
CC	detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are		
CC	useful in gene therapy, for developing a diagnostic marker or medicines		
CC	for regulating their expression and activity, or as a target of gene		
CC	therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides		
CC	are useful as pharmaceutical agents. The present sequence represents a		
CC	cDNA sequence of the invention.		
XX	Sequence 3466 BP; 780 A; 985 C; 1005 G; 696 T; 0 U; 0 Other;		
SQ			

Query Match	85.1%	Score 2644.2	DB 11	Length 3466
Best Local Similarity	91.9%	Pred. No. 0		
Matches 2931	Conservative 0	Mismatches 3	Indels 255	Gaps 3
Qy	1	ATGCTACGAAACCGCAGGACGCGGCTCTGTGCGCTGTCCACTACTTGGAGAACTC	60	
Db	145	ATGCTACGAAACCGCAGGACGCGGCTCTGTGCGCTGTCCACTACTTGGAGAACTC	204	
Qy	61	GAGGCTGTGGAACCTGAAGAAAGTTCAAGTTATACCTGGGGACCGCGACAGAGCTGGGAGAA	120	
Db	205	GAGGCTGTGGAACCTGAAGAAAGTTCAAGTTATACCTGGGGACCGCGACAGAGCTGGGAGAA	264	
Qy	121	GGCAAGATCCCTCGGGAAGCATGGAGAAAGCCGGTCCCTCTGGAAATGGGCCAGCTGCTC	180	
Db	265	GGCAAGATCCCTCGGGAAGCATGGAGAAAGCCGGTCCCTCTGGAAATGGGCCAGCTGCTC	324	
Qy	181	ATCACCCACTTTCGGCCAGAGGAGGCTGGAGGTTGGCTCTCAGCACTTTGAGCGGATA	240	
Db	325	ATCACCCACTTTCGGCCAGAGGAGGCTGGAGGTTGGCTCTCAGCACTTTGAGCGGATA	384	
Qy	241	AACAGGAAGGACCTGTGGGACAGAGGACAGAGAGGACCTGGTGGAGG	288	
Db	385	AACAGGAAGGACCTGTGGGACAGAGGACAGAGAGGACCTGGTGGAGGATA	444	
Qy	289	-----	288	
Db	445	GGTGGCCGCTCCTCACTTGGGAACCACTCAACATGCCTTCTGGAAGTCTCTCTTGTCACT	504	
Qy	289	-----GATCCCGCAGGAACCTACAGGGACTATGTCCGCAGGAAATTCGGCTCATG	339	
Db	505	CCAAGAAAAGATCCCGCAGGAACCTACAGGGACTATGTCCGCAGGAAATTCGGCTCATG	564	
Qy	340	GAAGACCGCAATGCGCCTAGGCGGAATGTCTCAACCTCAGCCACCGGTACACCCGGCTC	399	
Db	565	GAAGACCGCAATGCGCCTAGGCGGAATGTCTCAACCTCAGCCACCGGTACACCCGGCTC	624	
Qy	400	CTGCTGGTGAAGGAGCACTCAAAACCCCATGCAGTCCAGCAGCAGCTTCTGGACACAGGC	459	
Db	625	CTGCTGGTGAAGGAGCACTCAAAACCCCATGCAGTCCAGCAGCAGCTTCTGGACACAGGC	684	
Qy	460	CGGGGACACCGGAGGACCGTGGGACACGAGGCTAGCCCATCAAGATAGAGACCTCTTTT	519	
Db	685	CGGGGACACCGGAGGACCGTGGGACACGAGGCTAGCCCATCAAGATAGAGACCTCTTTT	744	
Qy	520	GAGCCACAGAGGAGCGCCCGAGCCACCGCGCACCGGTGTCTATGCAAGCGCGGCGAGGG	579	
Db	745	GAGCCACAGAGGAGCGCCCGAGCCACCGCGCACCGGTGTCTATGCAAGCGCGGCGAGGG	804	
Qy	580	ATAGGCAAGTCCATGCTGGCACACAAGGATGATGTGGACTGGGCGGACGGGAAGCTCTTC	639	
Db	805	ATAGGCAAGTCCATGCTGGCACACAAGGATGATGTGGACTGGGCGGACGGGAAGCTCTTC	864	
Qy	640	CAAGGACAGATTGATTATCTTCTTCAATCAACTGCAGGGAGATGAACAGAGTGCCACG	699	
Db	865	CAAGGACAGATTGATTATCTTCTTCAATCAACTGCAGGGAGATGAACAGAGTGCCACG	924	
Qy	700	GAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCTGAGCCACCGCGCTCTCCAG	759	
Db	925	GAATGCAGCATGCAAGACCTCATCTTCAGCTGCTGGCTGAGCCACCGCGCTCTCCAG	984	
Qy	760	GAGCTCATCCGAGTTCGCGAGCGCTCCTTTTTCATCATCGACGGCTTCGATGAGCTCAAG	819	
Db	985	GAGCTCATCCGAGTTCGCGAGCGCTCCTTTTTCATCATCGACGGCTTCGATGAGCTCAAG	1044	
Qy	820	CTTCTTTTCCACGATTCCTCAGGACCTGTGTCCTGTGGAGGAGAAACCGGCCACG	879	
Db	1045	CTTCTTTTCCACGATTCCTCAGGACCTGTGTCCTGTGGAGGAGAAACCGGCCACG	1104	
Qy	880	GAGCTGCTCTTAACAGCTTAATTCGGNAGAGCTGCTCCCTGAGCTATCTTTGCTCATC	939	
Db	1105	GAGCTGCTCTTAACAGCTTAATTCGGNAGAGCTGCTCCCTGAGCTATCTTTGCTCATC	1164	

Db	918		TGCAAGACCTCATCTTCAGCTGCTGGCCTGAGCCAGCGCCCTCTCCAGGAGCTCATCC	977	Db	1998	AGTTTATCCAGCAGGCCCTGAGCCATTTCCAGGTGATCGTGGTCAGCAACATTCCTCTCA	2057
Qy	770		GAGTTCCGAGCGCTCTCTTTTCATCATCGAGCGCTTCGATGAGCTCAAGCTCTTTTCC	829	Qy	1850	AGATGGAGCACATGCTCTCTCTGTTCTGTTGAAGCGCTGAGGAGCGCCAGGTGCTGC	1909
Db	978		GAGTTCCGAGCGCTCTCTTTTCATCATCGAGCGCTTCGATGAGCTCAAGCTCTTTTCC	1037	Db	2058	AGATGGAGCACATGCTCTCTCTGTTCTGTTGAAGCGCTGAGGAGCGCCAGGTGCTGC	2117
Qy	830		ACGATCTTCAGGACCCCTGCTGCTCTGCTGGAGGAAACGCGCCACCGAGCTGCTTC	889	Qy	1910	ACTTGTATGCGCCACCTACAGCGCGACCGGGGAAGACCGCGCGAGGTGCTCCGAGGAG	1969
Db	1038		ACGATCTTCAGGACCCCTGCTGCTCTGCTGGAGGAAACGCGCCACCGAGCTGCTTC	1097	Db	2118	ACTTGTATGCGCCACCTACAGCGCGACCGGGGAAGACCGCGCGAGGTGCTCCGAGGAG	2177
Qy	890		TTACAGCTTAATTCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATACACACGCG	949	Qy	1970	CGCACAGCTTGGTGGTCAGCTCAGACAGAGGAGCGGTCTGCTGAGCGCTTACAGTG	2029
Db	1098		TTACAGCTTAATTCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATACACACGCG	1157	Db	2178	CGCACAGCTTGGTGGTCAGCT---ACCAGAGGAGCGGTCTGCTGAGCGCTTACAGTG	2234
Qy	950		CCAGGCTTTCGGAAGCTCCACCGTCTGCTGGAGACCCCGAGGCATGTGGAGATCTGG	1009	Qy	2030	AACATCTGGCAGCGGCGCTGTGCACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGAA	2089
Db	1158		CCAGGCTTTCGGAAGCTCCACCGTCTGCTGGAGACCCCGAGGCATGTGGAGATCTGG	1217	Db	2235	AACATCTGGCAGCGGCGCTGTGCACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGAA	2294
Qy	1010		GCTTCTCTGAGGCAAGGAAGTAATTTCTACAAGTATTTCCACAATGACAGAGCAGG	1069	Qy	2090	ATGCCCTTGGCAGCGCGGGGTGAAGCTGTCTCTCAAGGACTCAGACACCCCAACTGCA	2149
Db	1218		GCTTCTCTGAGGCAAGGAAGTAATTTCTACAAGTATTTCCACAATGACAGAGCAGG	1277	Db	2295	ATGCCCTTGGCAGCGCGGGGTGAAGCTGTCTCTCAAGGACTCAGACACCCCAACTGCA	2354
Qy	1070		CGGSCCAAGCTTCAATTACGTGAGGACCAAGAGCTCTCTTCCACATGTCTTCTGTC	1129	Qy	2150	AACCTTCAGAACCTTGAGGCTGAAGAGGTGCGGCATCTCCAGCTCAGCCTGCGAGACCTCT	2209
Db	1278		CGGSCCAAGCTTCAATTACGTGAGGACCAAGAGCTCTCTTCCACATGTCTTCTGTC	1337	Db	2355	AACCTTCAGAACCTTGAGGCTGAAGAGGTGCGGCATCTCCAGCTCAGCCTGCGAGGACCTCT	2414
Qy	1130		CCCTGTGTGCTGGTGTGTACCTGCTCCAGCAGCAGCTGAGGGGTGGGGGCTGT	1189	Qy	2210	CTGCAGCTCTCATAGCCCAATAAGAAATTTTGACAGGATGGATCTCAGTGGGCAACGCGTTG	2269
Db	1338		CCCTGTGTGCTGGTGTGTACCTGCTCCAGCAGCAGCTGAGGGGTGGGGGCTGT	1397	Db	2415	CTGCAGCTCTCATAGCCCAATAAGAAATTTTGACAGGATGGATCTCAGTGGGCAACGCGTTG	2474
Qy	1190		TGACACAGACGCTCCAGGACCAACCACTGCAGGTACATGCTCTACCTGCTGAGTCTGATGC	1249	Qy	2270	GAITTCAGGATGATGCTCTCTTTTGGAGGGCTTGGCGGCATCCCCAGTGCAGGCTGCAGA	2329
Db	1398		TGACACAGACGCTCCAGGACCAACCACTGCAGGTACATGCTCTACCTGCTGAGTCTGATGC	1457	Db	2475	GAITTCAGGATGATGCTCTCTTTTGGAGGGCTTGGCGGCATCCCCAGTGCAGGCTGCAGA	2534
Qy	1250		AACCCAGCGGGGCGCGCCCTCCAGGCCCCACCCCAACAGAGAGGTTTGTCTCT	1309	Qy	2330	TGATTCAGTTGAGGAAGTGTACGTGAGTCCCGGGCTTGTACAGGATGCTCTCTGTCGC	2389
Db	1458		AACCCAGCGGGGCGCGCCCTCCAGGCCCCACCCCAACAGAGAGGTTTGTCTCT	1517	Db	2535	TGATTCAGTTGAGGAAGTGTACGTGAGTCCCGGGCTTGTACAGGATGCTCTCTGTCGC	2594
Qy	1310		TGGCGCAGATGGGCTCTGGAATCAGAAATCCTATTTGAGGACGAGCCTCCGGAAGC	1369	Qy	2390	TCGCGCAACCAACCAATCTGTTGAGTTGAGCTGACAGGAAATGCACTGGAGGATTTGG	2449
Db	1518		TGGCGCAGATGGGCTCTGGAATCAGAAATCCTATTTGAGGACGAGCCTCCGGAAGC	1577	Db	2595	TCGCGCAACCAACCAATCTGTTGAGTTGAGCTGACAGGAAATGCACTGGAGGATTTGG	2654
Qy	1370		ACGSCCTAGACGGGGAAGAGCTCTGCTCTTCTCAACATGAAATCTTCCAGAAAGCA	1429	Qy	2450	GCCTGAGGTTACTATGCGAGGACTGAGGCAACCCAGTCTCAGACTACGACTTTGTGTC	2509
Db	1578		ACGSCCTAGACGGGGAAGAGCTCTGCTCTTCTCAACATGAAATCTTCCAGAAAGCA	1637	Db	2655	GCCTGAGGTTACTATGCGAGGACTGAGGCAACCCAGTCTCAGACTACGAGCTTTGTGTC	2714
Qy	1430		TCAACTGTGAGAGTACTACAGCTTCATCCACTTGAAGTTCCAGGAATTTCTTTCAGCTA	1489	Qy	2510	TGAAGATCTCCGGCTCAGTCTGCTGCTGTGACGAGCTGGCTCAACTCTCAGTGTGA	2569
Db	1638		TCAACTGTGAGAGTACTACAGCTTCATCCACTTGAAGTTCCAGGAATTTCTTTCAGCTA	1697	Db	2715	TGAAGATCTCCGGCTCAGTCTGCTGCTGTGACGAGCTGGCTCAACTCTCAGTGTGA	2774
Qy	1490		TGTACTATCTCGAGGGGAGGGGCGGCGAGCCAGCCAGACGAGCTGACAGGC	1549	Qy	2570	ACCAGAGCTGAGAGAGCTGAGCTGAGCTGAGCTGAGCTGGGGGAGCTCGGGTGTGTC	2629
Db	1698		TGTACTATCTCGAGGGGAGGGGCGGCGAGCCAGCCAGACGAGCTGACAGGC	1757	Db	2775	ACCAGAGCTGAGAGAGCTGAGCTGAGCTGAGCTGAGCTGGGGGAGCTCGGGTGTGTC	2834
Qy	1550		TGTTGACCGAGTACGCGTTTCTGAAAGAGCTTCTTGGGACTCAGCAGCGCTTCTCTGT	1609	Qy	2630	TGCTGTGTGAGGGCTCAGGCATCCCAAGCTGCAAGCTTCCAGAGCCCTCGGTTGGGCTCT	2689
Db	1758		TGTTGACCGAGTACGCGTTTCTGAAAGAGCTTCTTGGGACTCAGCAGCGCTTCTCTGT	1817	Db	2835	TGCTGTGTGAGGGCTCAGGCATCCCAAGCTGCAAGCTCCAGAGCCCTC-----	2882
Qy	1610		TTGACTCTTGAAACGAGAGACAGGAGCCACTGGAGAGAGTCTTGTGGAGAGTCT	1669	Qy	2690	GCCGGCTGGGCTCTGCGGCTGTGAGGGTCTTCTGTGTGTGCTCCAGGCGCAACCAAC	2749
Db	1818		TTGACTCTTGAAACGAGAGACAGGAGCCACTGGAGAGAGTCTCTGCTGGAGAGTCT	1877	Db	2883	-----	2882
Qy	1670		CGCGCACATCAAGATGGAATGCTGTGAGTGGATCCAAAGCAAGCTCAGAGCGAGCT	1729	Qy	2750	TCCGGGAGCTGGACTTGAGTTTCAACGACCTGGGAGACTGGGGCTGTGTTGCTGGCTG	2809
Db	1878		CGCGCACATCAAGATGGAATGCTGTGAGTGGATCCAAAGCAAGCTCAGAGCGAGCT	1937	Db	2883	-----	2882
Qy	1730		CCACCTGACAGCGGCTCTTGTGAGTCTTTCAGCTGCTGTACAGATCCAGAGGAGG	1789	Qy	2810	AGGGGTGCAACATCCCGCTGCAGACTCCAGAAACTGTGGCTGGATAGCTGTGGCTCA	2869
Db	1938		CCACCTGACAGCGGCTCTTGTGAGTCTTTCAGCTGCTGTACAGATCCAGAGGAGG	1997	Db	2883	-----GGCTGGATAGCTGTGGCTCA	2903
Qy	1790		AGTTTATCCAGCAGCGCCTGAGCCATTTCCAGGTGATCGTGGTCAGCAACATTTGCTCCA	1849	Qy	2870	CAGCCAAGCTTGTGAGAAATCTTTTACCTCCCTGGGGATCAACAGACCTTGACCGACC	2959
Db					Db	2904	CAGCCAAGCTTGTGAGAAATCTTTTACCTCCCTGGGGATCAACAGACCTTGACCGACC	2963

QY 2930 TTTTACCTGACCAACAAGCCCTAGGGGACACAGGTTGTCGACTGCTTTGGCAAGCGGCTGA 2989
Db |||||||
QY 2964 TTTTACCTGACCAACAAGCCCTAGGGGACACAGGTTGTCGACTGCTTTGGCAAGCGGCTGA 3023
Db |||||||
QY 2990 GCCATCCTGGCTGCAAACTCCGAGTCTCTGTTTATTGGGATGGACCTGAATAAATGA 3049
Db |||||||
QY 3024 GCCATCCTGGCTGCAAACTCCGAGTCTCTGTTTATTGGGATGGACCTGAATAAATGA 3083
Db |||||||
QY 3050 CCACAGTAGTTGGCAGCGCTTCGAGTACAAACCTTATTGGACATTGGCTGCTGA 3108
Db |||||||
QY 3084 CCCACAGTAGTTGGCAGCGCTTCGAGTACAAACCTTATTGGACATTGGCTGCTGA 3142
Db |||||||

RESULT 12
ADP47729
ID ADP47729 standard; cDNA; 3221 BP.
XX AC
XX ADP47729;
XX DT
XX 12-AUG-2004 (first entry)
XX DE Human Monarch-1 (CATERPILLER 19.3) isoform IV cDNA.
XX KW Monarch-1; CATERPILLER 11.2; caspase recruitment domain;
KW CARD, transcription enhancer, R-binding, pyrin, lots of leucine repeat;
KW CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIAS1;
KW cold-induced autoinflammatory syndrome 1; antiinflammatory; cytosolic;
KW inflammatory disease; cancer; gene therapy; human; gene; ss; purine;
KW CATERPILLER 19.3; chromosome 19q13; multiple sclerosis; isoform IV.
XX OS Homo sapiens.
XX WO2004034093-A2.
XX PN
XX 22-APR-2004.
XX PD
XX PF 30-APR-2003; 2003WO-US013562.
XX PR 30-APR-2002; 2002US-0376626P.
XX PA (UYNC-) UNIV NORTH CAROLINA.
XX PI Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'connor W;
PI Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;
XX DR WPI; 2004-348215/32.
XX DR P-PSDB; ADP47730.
XX XX
XX PT New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3,
XX CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 polypeptide, useful in
XX PT preparing a composition for treating inflammatory disease or cancer.
XX PS Claim 4; SEQ ID NO 7; 205pp; English.
XX CC The invention relates to a novel isolated nucleic acid encoding a Monarch
XX -1, CATERPILLER (CARD [caspase recruitment domain], transcription
XX enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2,
XX CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 (cold-
XX induced autoinflammatory syndrome 1) polypeptide comprising the amino
XX acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or
XX its fragment. The nucleic acid of the invention demonstrates
XX antiinflammatory and cytostatic activities and may be useful in preparing
XX a composition for treating an inflammatory disease or cancer, possibly
XX via gene therapy. The current sequence is that of the human Monarch-1
XX (CATERPILLER 19.3) isoform IV cDNA of the invention which is located on
XX chromosome 19q13, in the multiple sclerosis susceptibility region.
XX SQ Sequence 3221 BP; 749 A; 891 C; 936 G; 645 T; 0 U; 0 Other;

Query Match 77.8%; Score 2417; DB 12; Length 3221;
Best Local Similarity 96.9%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 81; Gaps 1;

QY 1 ATGCTAGCAACCCAGCGACGGCGCTCTGTGCTCTTCCACCTACTTGGGAAGAACTC 60
Db |||||||
QY 61 GAGGCTCTGGAACTGAAGAAAGTTCAAGTTTATACCTGGGACCCGCGACAGAGCTGGGAGAA 120
Db |||||||
QY 281 GAGGCTCTGGAACTGAAGAAAGTTCAAGTTTATACCTGGGACCCGCGACAGAGCTGGGAGAA 340
Db |||||||
QY 121 GGCAAGATCCCTCTGGGGAAGCATGGGAAGCGGCTCCCTCGAAATGGCCAGCTGCTC 180
Db |||||||
QY 341 GGCAAGATCCCTCTGGGGAAGCATGGGAAGCGGCTCCCTCGAAATGGCCAGCTGCTC 400
Db |||||||
QY 181 ATACCCACATTCGGGCGCAGAGAGGCTTGAGGTTGGCTCTCAGCACCTTTTGAGCGGATA 240
Db |||||||
QY 401 ATACCCACATTCGGGCGCAGAGAGGCTTGAGGTTGGCTCTCAGCACCTTTTGAGCGGATA 460
Db |||||||
QY 241 AACAGGAAGACCTGTGGGAGAGAGGACAGAGAGAGCACTGGTGAGG----- 288
Db |||||||
QY 461 AACAGGAAGACCTGTGGGAGAGAGGACAGAGAGAGCACTGGTGAGGATACCCACCT 520
Db |||||||
QY 289 ----- 288
Db |||||||
QY 521 GGTGGCCCGTCTCATTGGGAAACAGTCAACATGCCTTCTGGAAGTCTCTTGTCACT 580
Db |||||||
QY 289 -----GATCCCCCAGGAAACCTACAGGACTATGTCCGAGGAAATTCGGGCTCATG 339
Db |||||||
QY 581 CCAAGAAAGATCCCCAGGAAACCTACAGGACTATGTCCGAGGAAATTCGGGCTCATG 640
Db |||||||
QY 340 GAAGACCGCAATGCGCGCTAGGGGAAATGTCTCAACCTCAGCCACCGGTACACCCGGCTC 399
Db |||||||
QY 641 GAAGACCGCAATGCGCGCTAGGGGAAATGTCTCAACCTCAGCCACCGGTACACCCGGCTC 700
Db |||||||
QY 400 CTGCTGGTGAAGGAGCACTCAAAACCCCATGCAAGTTCAGAGCAAGCTTTTGGACACAGGC 459
Db |||||||
QY 701 CTGCTGGTGAAGGAGCACTCAAAACCCCATGCAAGTTCAGAGCAAGCTTTTGGACACAGGC 760
Db |||||||
QY 460 CCGGGAACAGCGAGGACCGTGGGACACAGGCTAGCCCATCAGATAGAGACCTCTTT 519
Db |||||||
QY 761 CCGGGAACAGCGAGGACCGTGGGACACAGGCTAGCCCATCAGATAGAGACCTCTTT 820
Db |||||||
QY 520 GAGCCAGAGGAGGCGGCCCGGACACCGGCAACCGGTGTCATCAAGGCGCGCAGGG 579
Db |||||||
QY 821 GAGCCAGAGGAGGCGGCCCGGACACCGGCAACCGGTGTCATCAAGGCGCGCAGGG 880
Db |||||||
QY 580 ATAGGCAAGTCCATGCTGGCAACAAGGATGCTGGACTGGCGGACGGGAAGCTCTTC 639
Db |||||||
QY 881 ATAGGCAAGTCCATGCTGGCAACAAGGATGCTGGACTGGCGGACGGGAAGCTCTTC 940
Db |||||||
QY 640 CAAGGCAAGTTCATGATCTCTTCTACATCAACTGCAGGAGATGAACCCAGAGTGCACG 699
Db |||||||
QY 941 CAAGGCAAGTTCATGATCTCTTCTACATCAACTGCAGGAGATGAACCCAGAGTGCACG 1000
Db |||||||
QY 700 GAATGCAGATGCAAGACCTCATCTTTCAGTCTGGCCTGAGCCCGGCGGCTCTCCAG 759
Db |||||||
QY 1001 GAATGCAGATGCAAGACCTCATCTTTCAGTCTGGCCTGAGCCCGGCGGCTCTCCAG 1060
Db |||||||
QY 760 GAGCTCATCGAGTTCGAGGCGCTCTTTCATCATCATCGAGGCTTCGATGAGTCAAG 819
Db |||||||
QY 1061 GAGCTCATCGAGTTCGAGGCGCTCTTTCATCATCATCGAGGCTTCGATGAGTCAAG 1120
Db |||||||
QY 820 CCTTCTTTCCACGATCTCAGGACCTGCTGGTCTCTGCTGGGAGGAGAAACGGCCACG 879
Db |||||||
QY 1121 CCTTCTTTCCACGATCTCAGGACCTGCTGGTCTCTGCTGGGAGGAGAAACGGCCACG 1180
Db |||||||
QY 880 GAGCTGCTTTTAAAGCTTAATCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATC 939
Db |||||||
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Db |||||||
QY 1241 ACCACAGGCGCCCGGCTTTGGGAAGCTCCACCGTCTGCTGGAGCACCCACGAGCATGTG 1300
Db |||||||

The invention relates to a novel isolated nucleic acid encoding a Monarch-1, CATERPILLER (CARD (caspase recruitment domain), transcription enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2, CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIASI1 (cold-induced autoinflammatory syndrome 1) polypeptide comprising the amino acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or its fragment. The nucleic acid of the invention demonstrates anti-inflammatory and cytostatic activities and may be useful in preparing a composition for treating an inflammatory disease or cancer, possibly via gene therapy. The current sequence is that of the murine Monarch-1 (CATERPILLER 19.3) predicted DNA of the invention.

XX
SQ
Sequence 3102 BP; 750 A; 786 C; 872 G; 694 T; 0 U; 0 Other;

Query Match	60.0%	Score 1864.8	DB 12	Length 3102
Best Local Similarity	75.7%	Pred. No. 0		
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QY	61	GAGGCTGTGGAACTGAAGAAAGTTTCAAGTTTATACCTGGGGACCGGCACAGAGCTGGGAA	120	
DB	61	GAGCTGGGAACTGAAGAAATTCATTCCTGGGGATTGAGAGGACCTGAGCGAG	120	
QY	121	GGCAGATCCCTGGGAGACATCGAAGAGCGCGTCCCTGGAAATGGCCACGCTGCTC	180	
DB	121	GACAAAATTCCTGGGACGAAATGAGAGAGCTGGTCTCTGGAAATGGCTCAGCTGATG	180	
QY	181	ATCACCCACTTTCGGGCCACAGAGGACCTGGAGTTGGCTCTCAGACCTTTGAGCGGATA	240	
DB	181	GTGGCCACATGGGACAAAGGAGCTTGGCTCTGGGCTCTCAGACCTTTTCAGAGGATT	240	
QY	241	AACAGGAAGACCTGTGGAGAGGACACAGAGAGGACCTGGTGAGG- - - - -	288	
DB	241	CACAGGAAGGACCTGTGGAGCGGAGCAGGAGAGGACCTTGGTGAGGGGTAAAGAGGC	300	
QY	289	-----GATCCCCAGGAAACCTACAGGAGACTATGTCCGACGGAATTCGGGCTCATGAA	342	
DB	301	AAGGAGATCTACACACAACCTTACAAAGACTATGTCCGAAGGAATTCAGCTAATGAA	360	
QY	343	GAACGCAATGCGGCTTAGGGAAATGTCTCAACTCAGCCACCGGTACACCGGCTCTG	402	
DB	361	GACCCCAATGCAAGATTAGGCGAAATGTGTGAACCTGAGCAATCGTTTACCTCGGCTTCTC	420	
QY	403	CTGGTGAAGGAGCACTCAAAACCCCATGCAAGTCCAGCAGCAGCTTCTGACACAGCCGG	462	
DB	421	CTAGTAAAGAACACTCAAACTCTATCTGGACACAGCAGAAATTTGTAGATGAGTGG	480	
QY	463	GGACACGCGAGGACCGTGGGACACAGGCTAGCCCATCAAGATAGACCTCTTTGAG	522	
DB	481	GAACGCTCAGAAACAGGCGTCACACAGCTAGTCTCTATCCAAATGGAGACCTCTTTGAG	540	
QY	523	CCAGACGAGGCGCCCGAGCCACCGCCACCGTGTCTCATGCAAGGCGCGCAGGGATA	582	
DB	541	CCAGACGAGAAACGCCCCGAGCCACACACAGTGTATTACAGGGGCGCGGGGATG	600	
QY	583	GGCAAGTCCATGCTGGCACACAGGTGATCTGGACTGGGCGGACGGGAAGCTTTCGAA	642	
DB	601	GGGAAGTCCATGCTGGCCCCACAAAGTGTGTGGACTGGGCGCGATGGGAGGCTTTCGAA	660	
QY	643	GGCAGATTGATTTATCTCTCTACATCAACTGCAGGGAGATGAACACAGAGTGCCACGGAA	702	
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DB	721	TGCAGGTGACAAACCTCATCTCCAGCTGTGGCCGAGCGTGGTATATCCCTCGAAGAC	780	
QY	763	CTCATCGAGTTCCGAGCGCTCTCTTTTCATCATCGAGGCTTCGATGAGCTCAAGCCT	822	
DB	781	CTCATGAGGCTCTGACCGCTCTCTTATCATATTGATGGCTTCGAAATACCTCATCTCT	840	

Db 1621 TGTGAGGCTCTTTGTGGTCTCCAGGCCAACACCACTCCGGGAGCTGCACTTGAAT 1680
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Qy 2830 TGCAGACTCCAGAACTGTGG 2850
Db 1741 TGCAGACTCCAGAACTGTGG 1761
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XX ABS78719;
AC ABS78719;
XX
DT 16-DEC-2002 (first entry)
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DE Human cDNA encoding NAAP9, from INCYTE no.429930CB1.
XX
KW Human; ss; gene; nucleic acid associated protein; NAAP; cancer;
KW cell proliferative disease; cancer; atherosclerosis; hepatitis;
KW neurological disorder; Parkinson's disease; Alzheimer's disease; stroke;
KW epilepsy; developmental disorder; renal tubular acidosis; anaemia;
KW glaucoma; hypothyroidism; autoimmune disorder; AIDS;
KW inflammatory disorder; acquired immunodeficiency syndrome; allergy;
KW atopic dermatitis; arthritis; bacterial infection; viral infection;
KW parasitic infection; protozoal infection; fungal infection.
XX
OS Homo sapiens.
XX
XX WO200272630-A2.
XX
PD 19-SEP-2002.
XX
XX 07-FEB-2002; 2002WO-US003844.
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XX 09-FEB-2001; 2001US-0268118P.
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PR 21-FEB-2001; 2001US-0270963P.
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PR 22-FEB-2001; 2001US-0270858P.
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PR 23-FEB-2001; 2001US-0271194P.
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PR 12-APR-2001; 2001US-0283496P.
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PR 09-NOV-2001; 2001US-0344650P.
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XX (INCY-) INCYTE GENOMICS INC.
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XX Thornton M, Hafalia AJA, Lu DAM, Arvizu C, Swarnakar A, Lu Y;
PI Warren BA, Baughn MR, Tang YT, Lee EA, Yao MG, Ramkumar J, Khan FA;
PI Gandhi AR, Ding L, Yue H, Gietzen KJ, Wallia NK, Thangavelu K;
PI Elliott VS, Marquis JP;
XX
XX WPI; 2002-723320/78.
DR P-PSDB; ABG97475.
XX
XX New human nucleic acid-associated proteins (NAAP), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant NAAP expression, e.g. cancer, hepatitis, AIDS, atherosclerosis,
PT infections.
XX
XX Claim 5; Page 160; 162pp; English.
XX
XX The invention relates to an isolated polypeptide comprising one of 10
CC human nucleic acid associated protein (NAAP1-10), or a biologically
CC active or immunogenic fragment of the polypeptide, and their encoding
CC nucleic acid. Also included are a recombinant polynucleotide comprising a
CC promoter sequence operably linked to the polynucleotide, a cell
CC transformed with the recombinant polynucleotide, a transgenic organism
CC comprising the recombinant polynucleotide, an anti-NAAP antibody,
CC screening for a compound that is effective as an ant/agonist or modulator
CC of NAAP, generating an expression profile of a sample containing the

CC polynucleotides and an array comprising different nucleotide molecules
CC affixed on a solid substrate, nucleotide molecule comprises a first
CC oligonucleotide or polynucleotide sequence specifically hybridizable with
CC at least 30 contiguous nucleotides of the target (NAAP) polynucleotide.
CC The polypeptides and polynucleotides are useful in diagnosing, treating
CC and preventing diseases or conditions associated with the decreased
CC expression or overexpression of NAAP, such as cell proliferative diseases
CC (e.g. cancer, atherosclerosis, hepatitis), neurological disorders
CC (Parkinson's disease, Alzheimer's disease, stroke, epilepsy),
CC developmental disorders (renal tubular acidosis, anaemia, glaucoma,
CC hypothyroidism), autoimmune/inflammatory disorders (AIDS (acquired
CC immunodeficiency syndrome), allergies, atopic dermatitis, arthritis) and
CC infections (e.g. bacterial, viral, parasitic, protozoal, fungal) and many
CC other diseases and disorders listed in the specification. These are also
CC useful in assessing the effects of exogenous compounds on the expression
CC of nucleic acid and amino acid sequences of NAAP. The NAAP or its
CC fragments are useful in screening compounds for effectiveness as agonist
CC or antagonist of the polypeptides, or in altering the expression of the
CC target polynucleotide and compounds that specifically bind to or modulate
CC the activity of the polypeptide. The microarray is useful in monitoring
CC or measuring protein-protein interactions, drug-target interactions, and
CC gene expression profiles. The present sequence encodes an NAAP protein
XX
XX Sequence 2158 BP; 489 A; 578 C; 639 G; 452 T; 0 U; 0 Other;
SQ
Query Match 54.1%; Score 1681.8; DB 6; Length 2158;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
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Db 181 GCACCTACCAAGCGCTTCTGTTTGGACTCTCTGAAAGAGAGACAGAGACCCAGCTGAG 240
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Qy 1768 TTGTACGAGATCCAGAGGAGGAGTTTATCCAGAGGCGCTCGAGCCACTTCCAGGTGATC 1827
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Db 421 GTGGTCAGCAACATTCGCTCCAGAGTGGAGCAGATGCTCTCCTGCTCTCTGTAAGCGC 480
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Db 541 CGCGGAGGTGCTCCGAGAGGCGCAGACGCTGTTGGTGCAGCTCAGACAGAGAGAGACC 597
Qy 2008 GTTCTGCTGAGCGCTTACAGTGAACATCTGGCAGCGCGCTGTCACCATCCAAACCTG 2067
Db 598 GTTCTGCTGAGCGCTTACAGTGAACATCTGGCAGCGCGCTGTCACCATCCAAACCTG 657

us-10-781-294-23.rng

Wed Feb 9 10:22:12 2005

Search completed: February 8, 2005, 16:38:28
Job time : 1538 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
9686.758 Million cell updates/sec

Title: US-10-781-294-23

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	398	12.8	4556	4	US-09-388-221B-9
3	395.8	12.7	4200	4	US-09-388-221B-3
4	395.8	12.7	4332	4	US-09-388-221B-5
5	395.8	12.7	4466	4	US-09-388-221B-11
6	299	9.6	1371	2	US-08-910-731-1
7	299	9.6	1371	2	US-08-795-395-1
8	293.2	9.4	1371	2	US-08-910-731-7
9	272.6	8.8	1386	2	US-08-910-731-5
10	256.6	8.3	1374	2	US-08-910-731-3
11	256.6	8.3	1374	2	US-08-795-395-3
12	85.8	2.8	257	4	US-09-016-434-208
13	83.2	2.7	376	4	US-09-023-655-395
14	77.4	2.5	678	4	US-09-016-434-1011
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16	68.2	2.2	4485	4	US-10-014-269-1
17	68.2	2.2	4486	4	US-10-014-269-33
18	68.2	2.2	39936	4	US-09-949-016-14951
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45	58	1.9	4366	4	US-09-064-199-14	Sequence 14, Appli

ALIGNMENTS

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; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4422)
US-09-388-221B-1

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Db 1568 CTTGGCTGGCTGCACTTGGCTGATGTCAGCAGATGAAGCGGAAGAAAACCTCACATGA 1627
Qy 1199 CGTCAGGACCACTGCACTGTACATGCTCTACCTGCTGAGTCTGATGCAACCCCAAGC 1258
Db 1628 CTTTCAAGACCAACCAACCTCTGTCTAATTAACCTTGGCCAGGCTCTCAGCTCAGC 1687
Qy 1259 CGGGGGCCCGCGCTCCAGCCCCCACCACAGAGAGGGTGTGCTCTTGGCGGCGAG 1318
Db 1688 CATTTGG-----GACCCAGCTCAGAGACCTCTGCTCTCTGGCTGCTG 1729
Qy 1319 ATGGGCTCTGAATCAGAAATCTATTTAGGAGCAGGAGCTCCGGAAGCAGCGCTAG 1378
Db 1730 AGGGCATCTGGCAAAAAGAACCTTTTTCAGTCCAGATGACCTCAGGAAGCATGGGTTAG 1789
Qy 1379 ACGGGGAAGCTCTCTGCTTCTCAACATGAACATCTCCAGAGGACATCAACTGTG 1438
Db 1790 ATGGGGCCATCATCTCAACCTCTTTGAAGATGGGTATTTCTTCAAGAGCACCCCATCCCTC 1849
Qy 1439 AGAGGTACTACAGCTTCATCACTTGATTTCCAGGAATCTTTGCACTATGTACTATA 1498
Db 1850 TGAG--CTACAGCTTCATTCACTCTGTTTCCAAAGAGTTCTTTGCAAGAAATGTCCTATG 1906
Qy 1499 TCCTGGACGGGGAGGGCGGGGAGCCAGACCCAGAGAGCTGACAGGCTGTGTGACCG 1558
Db 1907 TCTTGGAGGATGAGAAGGGGAGAGGTAAACATTTCTAATTGATCATAGATTTGGAAGA 1966
Qy 1559 AGTACGCTTTTCTGAAGGAGCTTCCT-----GGCACTCACAGCGCTTCCTGTTTG 1612
Db 1967 CGCTAGAAGCATATGGAATACATGGCTGTGGGGCATCAACACAGCTTCTCTATTTGG 2026
Qy 1613 GACTCTTGAACAGGAGACCAAGGACCACTGGAGAGAGTCTCTGCTGGAAGGTCTCGC 1672
Db 2027 GCCTGTTAAGTGATGAGGGGAGAGAGATGGAGAACATCTTTCACTGCGCGGTGCTC 2086
Qy 1673 GGCACATCAAGATGACCTGTGATGGATCCAAAGCAAGCTCAGAGGACGGCTCCA 1732
Db 2087 AGGG-----GAGGAACCTGATGCAGTGGGTCCCGTCCCTCGAGCTGCT----- 2129

Qy 1733 CCCTGCAGCAGGGCTCCTTGGAGTTCTTACGCTGCTTTGTATACGAGATCCAGGAGGAGGT 1792
Db 2130 -GCTGCAGCCACACTCTCTGAGTCCCTCCTCCTGCTTGTACGAGATCGGAACAAAAGCT 2188
Qy 1793 TTATCCAGCAGGGCCCTGAGCCTTCCAGGTGATGCTGGTCAGCAACATTTGCTCTCAAGA 1852
Db 2189 TCCTGACACAAGTGTATGGCCCATTTTCGAAGAAA---TGGGATGTGTGTAGAAAACAGACA 2245
Qy 1853 TGGAGACATGCTCTCTCTGCTGCTGAAGCGCTGCAGAGCGCCAGCTGTGCACT 1912
Db 2246 TGGAGCTCTTAGTGTGCACTTTCTGCATTAATTCAGCCCGCAGTGAAGAGTTTCAGC 2305
Qy 1913 TGTATGCGCCACCTACAGCGCGAGCGGGAAGACCCGCGAGGTGCTCCGCGAGAGCGC 1972
Db 2306 TGATT-----GAGGGCAGGACGACAGATCAACATGGAGCC 2341
Qy 1973 ACAGCTGTTGGTGCAGCTCAGACCAGAGAGGACCGTTTGTGTGGACGCTTACAGTGAAC 2032
Db 2342 CCACCATGTTAGTCTCTGTTTCAG-----GTGGGTCCCAAGTCACAGATGCTTATTTGGCAGA 2395
Qy 2033 ATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGATAGAGCTGCTCTGTACCGAAATG 2092
Db 2396 TTCTTCTCCGTCTCAAGGTCAACAGAAACCTGAAGGAGCTGGACCTAAGTGGAAACT 2455
Qy 2093 CCCTGGGACGCCGGGGGTGAAGCTGCTCTGTCAAGGACTCAGACACCCCAACTGCAAAAC 2152
Db 2456 CGCTGAGCCACTCTGCAGTGAAGAGTCTTTTGAAGACCTTGAGACGCCCTCGCTGCCTCC 2515
Qy 2153 TTCAAGAACCTGAGGCTGAAGAGGTGCCGATCTCAGCTCAGCTCAGCTCGAGAGACCTCTCTG 2212
Db 2516 TGGAGACCTTGCCTGCTGGCTGTGGCTTCAAGCTGAGGACTGCAAGGACCTTGCCT 2575
Qy 2213 CAGCTCTATAGCAATAAGAAATTTGAACAAGGATGATCTCAGTGGCAACGGCGTTGGAT 2272
Db 2576 TTGGGCTGAGAGCCAAACAGACCTGACCGAGCTGGACCTTGAGTTCAATGTGCTCAGG 2635
Qy 2273 TCCAGGACATGATGCTGCTTTTGGAGGGCTGGGGCATCCCGAGTCCAGGCTGCAGATGA 2332
Db 2636 ATGCTGGAGCCAAACACTTTTGCAGAGACTGAGACAGCCGAGCTGCAAGCTACAGGAC 2695
Qy 2333 TTCAAGTTGAGGAAGTGTGAGTGGAGTCCGGGGCTTGTCAAGAGATGGCTTCTGTGCTG 2392
Db 2696 TGCAGCTGGTCACTGTGGCTTCAAGTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2755
Qy 2393 GCACCAACCACTCTGTTGAGTTGAGCTGAGACCTGACAGGAAATGCACCTGAGGATTTGGGCC 2452
Db 2756 GTGCCAGCCCGCTGAAGGAGCTAGACCTGACAGCAAGAACCTGGATGACGTTGGCG 2815
Qy 2453 TGAGGTTTACTATGCGAGGAGCTGAGGCAACCCAGTCTGAGACTACGAGCTTTTGTGGCTGA 2512
Db 2816 TGGCACTGCTCTGTGAGGGGCTCAGGATCTCTGCTGCAAACTCATACGCTGGGGCTGG 2875
Qy 2513 AGATCTGCCCGCTCACTGCTGCTGCTGTGACAGAGCTG 2550
Db 2876 ACCAGAACACTCTGAGTGTATGATGAGGAGGAACTG 2913

RESULT 3

US-09-388-221B-3
; Sequence 3, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; FILE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4200
; TYPE: DNA

Wed Feb 9 10:22:12 2005

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4197)
; US-09-388-221B-3

Query Match      12.78; Score 395.8; DB 4; Length 4200;
Best Local Similarity 54.08; Pred. No. 2.2e-95;
Matches 1060; Conservative 0; Mismatches 822; Indels 81; Gaps 9;

QY 539 CCGAGCCACCGCGCACCGTGGTATGCAAGCGCGGAGGATAGCAAGTCCATGCTGG 598
DB 971 CCCAAGAACCTCGCATAGTCATCTGCGAGGGGCTGTGGAATTGGAAAGTCAACACTGG 1030
QY 599 CACACAGGTGATCTGGATGGCGGACCGGAGGCTTCCAAAGCAGATTGATTATC 658
DB 1031 CCAGCGAGGTGAAGAAAGCCCTGGGGGAGAGCCAGCTGTATGGGACCGCTTCCAGCATG 1090
QY 659 TCTTCTACATCAACTGCGAGGAGATGAACAGAGTGCACGGAATGCGAGATGCAAGACC 718
DB 1091 TCTTCTACTTCAGCTGCGAGAGCTGGCCAG---TCCAAGGTGGTGAAGTCTCGCTGAGC 1147
QY 719 TCATCTTCAGCTGCTGGCTGAGCCAGCGGCTCTCCAGGAGCTCATCCGAGTTCCTCG 778
DB 1148 TCATCGGAAAGATGGGACACCCACTCGGCTCCCATATAGACAGATCTCTTAGGCCAG 1207
QY 779 AGCGCTCTCTTTCATCATCGACGCTTCGATGAGCTCAAGCCCTTCTTTCCAGATCCTC 838
DB 1208 AGCGCTGCTCTTTCATCTCGATGGTGTAGATGAGCCAGGATGGTCTTTCAGAGCCGA 1267
QY 839 AGGAGCCCTGFGCTCTGCTGGGAGAGAAACCGGCCACCGAGCTCTTCTTAAAGCT 898
DB 1268 GTTCTGAGCTCTGTCTGCACTGGAGCCACACAGCCGCGGAGTGCATGCTGGGCGATT 1327
QY 899 TAAATTCGAGAGAGTGTCTCTGAGCTATCTTGTCTCATCACACAGCGGCCACCGCTT 958
DB 1328 TGTGGGGAAGAACTATCTTCCGAGGATCTTCTCTGATCACGGCTCGGACACAGCTC 1387
QY 959 TGGAGAAGCTCCACCGTCTGCTGGAGCACCCAGGCACTGTGGAGATCTTGGGCTTCTCTG 1018
DB 1388 TGCAGAACCTCATCTCTTTGGAGCAGGACGTTGGGTAGAGTCTCTGGGGTCTCTG 1447
QY 1019 AGCGAAGAGGAGGATCTCTACAGTATTTCCAAATGACAGCAGCGGCGGCAAG 1078
DB 1448 AGTCCAGCAGGAAGGAATATTTCTACAGATATTTACAGATGAAGGCAAGCAATTAG 1507
QY 1079 TCTTCAATTACGTGAGGGAACAAGGCTCTCTTCAACATGCTGTCTGCTCCCTGGTGT 1138
DB 1508 CTTTAGGTGGTCAATCAAAACAAAGAGCTCTGGGCCCTGTGTCTTGTGCTGGGTGT 1567
QY 1139 GCTGGGTGGTGTGTACTGCTCCAGCAGCTGGAGGGTGGGGGCTGTTGACACAGA 1198
DB 1568 CTTGGCTGGCTGCACTTGCTGATGACGAGATGAAGCGGAGGAAATCTCACATGA 1627
QY 1199 GTCCAGAGCACCACTGCACTGTACATGCTCTACCTGTCTGAGTCTGATGCAACCAAGC 1258
DB 1628 CTTTCAAGACACCAACCACTCTGTCTACATTAACCTTGCCAGGCTCTCCAAGCTCAG 1687
QY 1259 CGGGGGCCCCGCGCTCCAGCCCCCACCACAGAGAGGTTGTCTCTTGGGGGAG 1318
DB 1688 CATTTGG-----GACCCAGCTCAGAGACCTCTCTCTCTGCTGCTGCTG 1729
QY 1319 ATGGGCTCTGAATCAGAAATCCTATTGAGGAGCAGGACCTCCGGAAGCAGCGGCTAG 1378
DB 1730 AGGGCATCTGCAAAAAAAGACCCCTTTTCTAGTCCAGTACCTCAGGAGCATGGGTAG 1789
QY 1379 ACGGGGAAGAGCTCTCTGCTCTCTCAACATGAATCTTCCAGAGGACATCAACTGTG 1438
DB 1790 ATGGGGCCATCATCTCCACCTTCTTGAAGATGGGTATTTCTTCAAGAGCACCCCATCCCTC 1849
QY 1439 AGAGTACTACAGCTTCTACCTGATTTCCAGGAATCTTTTGGAGCTATGTACTATA 1498
DB 1850 TGAG---CTACAGCTTCATTCACTCTGTCTTCCAGAGTCTTTTGGAGCAATGCTCTATG 1906

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RESULT 4

US-09-388-221B-5

; Sequence 5, Application US/09388221B

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QY 1499 TCCTGGACGAGGGGAGGCGGCGGAGGCCAGAGCCAGGACCTGACCGGCTGTTGACCG 1558
DB 1907 TCTTGGAGGATGAGAAGGGGAGAGGTAAACAATCTTAATTGCAATCATAGATTTTGGAAGA 1966
QY 1559 AGTACGCGTTTCTGAAAGGAGCTTCTCT-----GGCACTACCAAGCCCTCTCTGTTTG 1612
DB 1967 CGCTAGAGCATATGGNATACATGCGCTGTGTTGGGCAATCAACCAACACGTTTCTTATTGG 2026
QY 1613 GACTCTTGAACGAGGAGACAGGAGCCACTTGGAGAGAGTCTCTGCTGGAAAGGCTCTCGC 1672
DB 2027 GCCTGTTAAGTGTAGTGGGGGAGAGAGATGAGAAACATCTTTTCACTGCGCGCTCTCTC 2086
QY 1673 CGCACATCAAGATGGACCTCTTGCAGTGTGATCCAAAGCAAGCTCAGAGCGAGCGGTCCA 1732
DB 2087 AGGG-----GAGNAACCTGATGCAATGGGTCCCGTCCCTGCAAGTGC----- 2128
QY 1733 CCCTGACGAGGGCTCTTGGAGTTCCTTCACTGCTTGTACGAGATCCAGGAGGAGGAGT 1792
DB 2129 TGCTGACGACACACTCTCTGAGTCCCTCCACTGCTTGTACGAGACTCGGAACAAACGCT 2188
QY 1793 TTATCCAGCGGCTTCCAGCTGATCGTGTGTCAGCAACATTTGCGCTCCCAAGA 1852
DB 2189 TCCTGACACAAAGTATGGCCCATTTTGAAGAA---TGGGCATGTGTAGAAACAGACA 2245
QY 1853 TGGAGCATATGCTCTCTCTGTTCTGTGTAAGCGCTCCAGGAGGCGCCAGGTCTGCACT 1912
DB 2246 TGGAGCTCTTAGTGTGCACTTTCTGCAATTAATTCAGCCCGCAGCTGAAGAGCTTCGCG 2305
QY 1913 TGTATGGCGCCACCTACAGCGCGGAGAACCCGCGAGGTGTCTCGCGAGGAGCGC 1972
DB 2306 TGATT-----GAGGCGAGGACGACAGATCAACATGGAGCC 2341
QY 1973 ACACGCTGTTGTGAGCTCAGACGAGAGGACCGTTCTGCTGGAGCGCTTACAGTGAAC 2032
DB 2342 CCACCATGTTGCTCTGTTTCTAG-----GTGGGTCCCAGTCAAGATGCTTATTTGGCAGA 2395
QY 2033 ATCTGGCAGCGGCTCTGTGCAACCAATCCAAACCTGATAGAGTGTCTGTACCGGAAATG 2092
DB 2396 TTCTCTTCTCTCTCTCAAGGTCACCAAGAACCTGAGAGAGCTGAGACTAAGTGGAACT 2455
QY 2093 CCTTGGGAGCGCGGGGTGAAAGCTGTCTCTCAAGGACTCAGACACCCCAACCTGCAAC 2152
DB 2456 CGCTGAGCCACTCTGAGTGAAGAGTCTTTTGAAGACCTGAGACGCTCTGCTGCTCTCC 2515
QY 2153 TTCAGAACCTGAGGCTGAAAGAGTGGCGCATCTCCAGCTCAGCTCGCGGAGGACCTCTCTG 2212
DB 2516 TGGAGACCTTGGGCTGCTGCTGCTTGGGCTTCAAGCTGAGGACTGCAAGGACCTTGCT 2575
QY 2213 CAGCTCTCATAGCCAAATGAATTTTGAACAAGGATGATCTCAGTGGCAACCGCGTGGAT 2272
DB 2576 TTGGGCTGAGAGCCACCAAGACCTTGAACCGAGCTGGACCTGAGTTCATATGTCTCACGG 2635
QY 2273 TCCAGGACATGATGCTGCTTTTGGAGGGCTTGGGATCCCAAGTGCAGGCTGCAAGTGA 2332
DB 2636 ATGCTGGAGCCAAACACCTTTTGGCAGAGACTGAGACAGCGAGCTGCAAGCTACAGGAC 2695
QY 2333 TTTAGTTGAGAGTGTACAGTGGAGTCCGGGCTTGTTCAGGAGATGGCTTCTGTGCTCG 2392
DB 2696 TGCAGCTGGTCACTGTTGGCTTCAAGTCTGACTGTCTGCTGCGAGGACCTGGCTCTGTCTTA 2755
QY 2393 GCACCAACCAACATCTGTTGAGTGGACCTGAGAGAAATGACATGAGAGATTTGGGCC 2452
DB 2756 GTGCGAGCCCGAGCTGAAGGAGCTAGACCTGACGAGAACAACTGGATGACGTTGGCG 2815
QY 2453 TGAGGTTACTATGCGAGGAGTGGGACCCAGCTCTGCAAGCT 2495
DB 2816 TGCAGTCTCTGTGAGGGGCTCAGGACATCTCTGCTGCAAACT 2858

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Patent No. 6818750
GENERAL INFORMATION:
APPLICANT: Reed, John C.
TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
FILE REFERENCE: P-LJ 3650
CURRENT APPLICATION NUMBER: US/09/388,221B
CURRENT FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 4332
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(4332)
US-09-388-221B-5

Query Match 12.7%; Score 395.8; DB 4; Length 4332;
Best Local Similarity 54.0%; Pred. No. 2.3e-95;
Matches 1060; Conservative 0; Mismatches 822; Indels 81; Gaps 9;

Qy	539	CCGAGCCACCGCCACCGTGTCTATGCAAGCGCGGAGGATAGGCAAGTCCATGCTGG	598
Db	971	CCCAAGAACCTCGCATAGTCTATCTGCGAGGGGGTGTGGAAATTTGGGAAGTCAACACTGG	1030
Qy	599	CACAAAGGTGATGCTGAGCTGGCGGACGGGAAGCTCTTCCAAAGGCAGATTTCATTATC	658
Db	1031	CCAGCGAGGTGAAGAACCTTGGGGGAGAGCCAGCTGTATGGGGACCGCTTCCAGCATG	1090
Qy	659	TCTTCTATCACTGCGAGGAGATGAACCAAGAGTGGCCACGGAATGAGCATGCAAGACC	718
Db	1091	TCTTCTACTTCAGCTGCAGAGAGCTGGCCAG---TCCAAAGTGTGAGTCTCGCTGAGC	1147
Qy	719	TCATCTTCACTGCTGGCTGAGCCAGCGGCTCTCCAGGAGCTCATCGAGTTCGG	778
Db	1148	TCATCGGAAAAGATGGGACAGCCACTCGGCTCCCATTTAGACAGATCTGTCTAGGGCAG	1207
Qy	779	AGCCCTCTCTTTCATCATCAACAGGCTTCGATGAGCTCAAGCCTTCTTCCACGATCCTC	838
Db	1208	AGCGCTGCTCTTCACTCTCATGCTGTGTAGATGAGCCAGGATGGGTCTTGAGAGCGGA	1267
Qy	839	AGGACCCCTGGTGTCTGTGGGAGGAGAAACGGCCCAACGGAGCTGCTTCTTAAACAGCT	898
Db	1268	GTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCGCGGAGTGCATGCTGGGCAATT	1327
Qy	899	TAATTCGAGAAAGCTGCTCCTGAGTATCTTTGCTCATCAACAGAGGCCCAAGGCTT	958
Db	1328	TGCTGGGGAAACTATATCTCCGAGGCATCTTCTCTGATCAGCGGCTCGGACCAAGCTC	1387
Qy	959	TGGAGAAGCTCCACGCTGCTGTGAGACACCCAGGCATGTGGAGATCTGGGCTTCTCTG	1018
Db	1388	TGCAGAACCTCATCTCTTTGAGAGAGGACGCTGGGTAGAGGTCTGGGGTCTCTG	1447
Qy	1019	AGGCAGAAAGAGGAATATCTTCAAGTATTTCCAAATGCAAGAGAGAGCGGGCCCAAG	1078
Db	1448	AGTCCAGCAGGAAGGAATATTTCTACAGATATTTACAGATGAAGCAAGCAATTAGAG	1507
Qy	1079	TCTTCAATTAGTGAAGGACAAAGAGCTCTCTTCAAGTGTCTGTCCTCCCTGGTGT	1138
Db	1508	CTTTAGGTGGTCAAAATCAAAAGAGCTCTGGGCGCTGTGTGTGGCTTGGGTGT	1567
Qy	1139	GCTGGGTGTGTACCTGCTCCAGCAGAGCTGGAGGTGGGGGTGTGTAGACAGA	1198
Db	1568	CCTGGCTGGCTGCACTTGGCTGTATGAGCAGATGAAGCGGAAGAAAACTCACTGA	1627
Qy	1199	CGTCCAGGACCAACCACTGCACTGATGCTCTACCTGCTGAGTCTGATGCAACCCCAAG	1258
Db	1628	CTTCCAGAGACCAACCAACCTCTGTCTACATTACCTTGGCCAGGCTCTCAAGCTCAGC	1687
Qy	1259	CGGGGGCCCGGCTCTCAGCCCCCAACCAACAGAGAGGGTGTGTCTCTTGGCGGAG	1318
Db	1688	CATTGG-----GACCCAGCTCAGAGACCTCTGCTCTCTGCTGCTG	1729

Qy	1319	ATGGGCTCTGGAATCAGAAAATCCTATTGAGGAGCAGGACCTCCGGAAGCAGCGCTAG	1378
Db	1730	AGGGCATCTGGCAAAAAAAGACCTTTTCAGTCCAGATGACCTCAGGAAGCATGGGTAG	1789
Qy	1379	ACGGGGAAGACGCT	1438
Db	1790	ATGGGGCCATCATCTCTCCACCTTCTTGAAGATGGGTATTTCTTCAAGACAGCAGCCAT	1849
Qy	1439	AGAGGTACTACAGCTTCACTCCAGTGTGAGTTTCCAGGAATTTCTTTGACGATGTACTATA	1498
Db	1850	TGAG---CTACAGCTTCATTCACCTCTGTTCGAAGAGTTCTTTGACGCAATGTCCTATG	1906
Qy	1499	TCCTGGAACGAGGGGAGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1558
Db	1907	TCCTTGGAGGATGAGAGGGGAGAGGTAAACATTTCTTATTCATCATAGATTTGGAAAAGA	1966
Qy	1559	AGTACGGGTTTTCTGAAAGGAGCTTCTCT-----GGCACTACACAGCGCTTCTCTGTTG	1612
Db	1967	CGCTAGAAGCATATGGAATACATGGCTGTGTGGGGCATCAACCAACGCTTTCCTATTGG	2026
Qy	1613	GACTCTGACGAGGAGACCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1672
Db	2027	GCCTGTTAAGTGTAGTGGGGGAGAGAGATGGAGAAACATCTTTCACTGCGCGCTGTCTC	2086
Qy	1673	CGACATCAAGATGGACCTGTTCAGTGGATCCAAAGCAAAAGCTTCAGAGCGACGGCTCCA	1732
Db	2087	AGGG-----GAGGAACCTGATGAGTGGGTCCCGTCCCTGCAGCTGC-----2128	
Qy	1733	CCCTGACGAGGCTCTCTGAGGTTCTTACGCTGCTTTGATAGAGTCCAGAGAGGAGT	1792
Db	2129	TGCTGACGACCACTCTCTGAGTCTCTCCACTGCTTGTACGAGCTCGGAACAAACGT	2188
Qy	1793	TTATTCAGCAGGCGGCTGAGCCACTTCCAGTGTATGCTGTGTCAGCAACATTCGCTCCA	1852
Db	2189	TCCTGACACAAGTGTATGGCCCATTTGGAAGAAA---TGGGCATGTGTGTAGAAAACAGA	2245
Qy	1853	TGAGACACATGTGCTCTCTGCTGAAGGCTGCAGAGCGGCGGCGGCGGCGGCGGCGGCT	1912
Db	2246	TGGAGCTCTTAGTGTGACCTTTCTGCAATTAATTCAGCCGCGGCGGCGGCGGCGGCT	2305
Qy	1913	TGTATGCGGCCACTTACAGCGCGGAGCGGGGAGAGCCGCGGAGGTGCTCCGAGAGCGG	1972
Db	2306	TGATTT-----GAGGGCAGGCGGAGCAGATCAACATGAGAGCC2341	
Qy	1973	ACAGCTGTTGGTGCAGCTCAGACGAGAGGAGCGGTTCTGCTGGAGCGCTTACAGTGNAC	2032
Db	2342	CCACATGGTGTGCTCTTTCAG-----GTGGGTCCAGTCCAGATGCTTATTTGGCAGA	2395
Qy	2033	ATCTGGCAGCGGCGGCTGTGCAACCAATCCAAACCTGATAGAGCTGCTCTGTACCGAAATG	2092
Db	2396	TTCT	2455
Qy	2093	CCCTGGGAGCGCGGGGGTGAAGTGTCTGTCAAGGACTCAGACACCCCAACTGCAAAAC	2152
Db	2456	CGCTGAGCCACTCTGCAAGTGAAGAGTCTTTGTAAGACCTTGGAGCGGCTCGCTGCTCC	2515
Qy	2153	TTCAGAACCTGAGGCTGAAGAGGTGCGCATCTCCAGCTCAGCTGCGGAGGAGCTCTCTG	2212
Db	2516	TGGAGACCTTGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2575
Qy	2213	CAGCTCTCATAGCCAAATTAAGAAATTTGACAAAGGATGAGTCTCAGTGGGCAACGGCGCT	2272
Db	2576	TTGGGCTGAGAGCCACAGACCTTGACCGAGCTGGAGCTTCAATGTGTCTCAGG2635	
Qy	2273	TCCAGGACATGATGCTGCTTTTGGAGGGCTGCGGCGATGCCAGTGTCCAGGTGAGATGA	2332
Db	2636	ATGCTGGAGCAAAACACCTTTTGCAGAGACTGAGACAGCGGAGCTGCAAGCTACAGGAC	2695
Qy	2333	TTCAAGTTGAGGAAGTGTACAGTGGAGTCCGGGGCTTGTGAGGAGATGGCTTCTGTGCTG	2392
Db	2696	TGACGTGGTGTGAGTGGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2755


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QY 2393 GCACCAACCCACATCTGGTTGAGTTGGACCTGACAGAAATGCACTGGAGGATTTGGGCC 2452
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2756 GTGCCAGCCCGCAGCTAGAGGAGCTAGACCTGCGAGAGAACACCTGGATGACGTTGGCG 2815
QY 2453 TGAGGTTACTATCCAGGAGCTGAGCAGCCAGCTCTGCAGACT 2495
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2816 TGGACTGCTCTGTGAGGGGCTCAGGCATCTGCTGCAACT 2858

RESULT 5
US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 4466
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4272)
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
; US-09-388-221B-11

Query Match 12.7%; Score 395.8; DB 4; Length 4466;
Best Local Similarity 54.0%; Pred. No. 2.3e-95;
Matches 1060; Conservative 0; Mismatches 822; Indels 81; Gaps 9;

QY 539 CCGAGCCACCGGACCGTGTGTCATGCAAGCGCGGAGGATAGGCAAGTCCATGCTGG 598
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
971 CCCAAGAACCTCGCATATCTGCAAGGGGGTGTGGAATGGGAAGTCAACACTGG 1030
QY 599 CACACAAGGTGATGTGACTGGGCGGACGGGAAGCTCTTCCAAAGGAGATTTGATATC 658
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1031 CCAGCAGGTGAGGAACCTGGGGAGAGCCAGCTGTATGGGACCGCTTCCAGCATG 1090
QY 659 TCTTCTCATCAATGCGAGGAGATGAACAGAGTGCACCGAATGCGATGCAAGACC 718
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1091 TCTTCTACTTCACTGTCAGAGAGCTGGCCAG---TCCAAAGTGGTGAAGTCTGCTGAGC 1147
QY 719 TCATCTTCAGCTGTGCGCTGAGCCAGCGCGCTCTCCAGGAGCTCATCCGAGTTCCTCG 778
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1148 TCATCGGAAGATGGAGACCACTCGGCTCCATAGACAGATCTGTCTAGGCGAG 1207
QY 779 AGCGCTCTCTTTTCATCATCGACGCTTCGATGAGCTCAAGCTTTTTCACGATCTC 838
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1208 AGCGCTGCTCTTCATCTCGATGTGTAGATGAGCCAGGATGGTCTTTCAGGAGCGGA 1267
QY 839 AGGAGCCCTGTGCTCTGCTGGGAGGAGAACCGCCACCGAGCTGCTTCTTAACAGCT 898
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1268 GTTCTGAGCTGTGCTGCACTGGAGCCAGCCAGCGCGGAGTGCATGCTGGGAGTT 1327
QY 899 TAATTCGGAAGAGTGTCTCTGAGCTATCTTTGCTCATCACACAGCGGCCACGGGCT 958
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1328 TGCTGGGAAACTATATCTTCCAGGAGCATCTTCTGATCAGGCTCGGACCAAGCTC 1387
QY 959 TGGAGAGCTCACCGTCTGTGAGAGACCCAGGAGATGTGGAGATCTTGGGCTTCTG 1018
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1388 TGCAGAACCTCATCTCTTTGGAGCAGGACGTTGGGTAGAGCTCTGGGGTCTCTG 1447
QY 1019 AGGAGAGGAGGAATATCTTCAAGTATTTCCAAATGTCAGACAGCGCGGCCAAG 1078
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1448 AGTCCAGCAGGAAGGAATATTTCTACAGATATTTTACAGATGAAGGACAGCAATTAGAG 1507

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QY 1079 TCTTCAATTTAGCTGAGGGACAAACGAGCTCTCTTCAACATGTGCTTCTGTCCTCCCTGGTGT 1138
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1508 CTTTAGTTGGTCAATCAACAAGAGCTCTGCGCCCTGTGTCTTGTGCTCCCTGGGTGT 1567
QY 1139 GCTGGTGGTGTGACCTGCTCCAGCAGAGCTGAGGGTGGGGGCTGTTGAGACAGA 1198
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1568 CTTGGCTGGCTGCACTTGTGATGACAGCAGATGAAGCGGAAGAAAACTCACACTGA 1627
QY 1199 GCTCCAGGACCACTGCTGCTGCTCTACCTGCTGAGTGTGATGCAACCCCAAGC 1258
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1628 CTTCCAGACCAACCAACCTCTGTGTACATTTACCTTGGCCAGGCTCTCAAGCTCAGC 1687
QY 1259 CGGGGGCCCGCGCTCCAGCCCAACCAAGAGAGGGTGTGCTCTTGGGCGAG 1318
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1688 CATTTGG-----GACCCAGCTCAGAGACCTCTGCTCTCTGGTGTCTG 1729
QY 1319 ATGGCTCTGGAATCAGAAATCTTATTTGAGGAGCAGGACCTCCGGAAGCAGCGCTAG 1378
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1730 AGGGCATCTGGCAAAAAAAGACCCCTTTTCACTTGAAGATGAGCTCAGGAAGCATGGGTAG 1789
QY 1379 ACGGGGAAGAGCTCTGCTGCTTCTCAACATGAACATCTTCCAGAAGGACATCAACTGTG 1438
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1790 ATGGGGCCATCATCTCCACCTTCTTGAAGATGGGTATTTCTTCAAGAGCACCCCATCCCTC 1849
QY 1439 AGAGGTACTACAGCTTTCATCCAGTATTCAGGAATTTCTTCCAGTATGTACTATA 1498
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1850 TGAG--CTACAGCTTCACTTCACTCTGTTTCCAAAGAGTCTTTTGCAGCAATGCTCTATG 1906
QY 1499 TCTTGAAGGGGGGAGGGGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1558
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1907 TCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1966
QY 1559 AGTAGCGGTTTCTGAAGGAGCTTCTCT-----GGCACTCACAGCGCTTCTGTTTG 1612
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1967 CGCTAGAGCATATGGAATACATGCTGTTTGGGGCATCAACACACAGCTTCTCTATTGG 2026
QY 1613 GACTCTGAAACAGAGAGACCGAGGAGCCTCGAGAGAGTCTTGTGTGAAGGTCTGCG 1672
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2027 GCTGTAAAGTGAATGAGGGGAGAGAGAGATGAGAAACATCTTCACTGCGGGTGTCTC 2086
QY 1673 CACACATCAAGATGAGACCTGTTGCAAGTGAATCAAAAGCAAGCTCAGAGCGAGGCTCCA 1732
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2087 AGGG-----GAGGAACCTGATGCAAGTGGTCCGCTCCCTGCGAGCTGC----- 2128
QY 1733 CCCTGACAGAGGCTCTTTGGAGTCTTTCAGTGTGTTTACAGATTCAGAGTTCAGAGGAGGAGT 1792
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2129 TGCTGACGACCACTCTCTGGAGTCCCTCCAAGTGTGACGAGCTCGGAAACAAACGT 2188
QY 1793 TTAATCCAGAGGCTGAGCCACTTCCAGTGTATGCTGTCAGAACATTTGCTCTCAAGA 1852
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2189 TCCTGACACAAGTGTGCGCCCATTTTGAAGAAA---TGGGCATGTGTGTAGAAACAGACA 2245
QY 1853 TGAGCAGATGCTCTCTGCTGTAAGCGCTGACAGGAGCGCCAGGCTGCTGCACT 1912
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2246 TGAGCTCTTAGTGTGCACTTTCTGCAATTAATTCAGCCGCGCAGCTGAAGAGCTTTCAGC 2305
QY 1913 TGTATGCGCCACTACAGCGGAGACCGCGGAGGAGTCTCCGAGGAGCGC 1972
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2306 TGATT-----GAGGGCAGGAGGAGCAGATCAACATGAGGAGC 2341
QY 1973 ACAGCTGTTGTTGACAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2032
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2342 CCACCATGTTGTTGTTGTTGAG-----GTGGGTCCAGCTCAGAGATGCTATTTGGCAGA 2395
QY 2033 ATCTGGCAGCGGCTGTGCAACCAATCAAACTGATAGAGTGTCTGTGACCGAAATG 2092
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2396 TTCTTCTCGCTCAAGGTCAACAGAAAACCTGAAGGAGCTGGACCTTAAGTGGAACT 2455
QY 2093 CCCTTGGCAGCGGGGGTGAAGTCTGTCTCAAGGACTCAGACACCCCAACTGCAAAAC 2152
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2456 CGCTGAGCCACTCTGCAAGTGAAGAGTCTTTTGAAGACCCCTGAGACCGGCTCGTGTGCTCC 2515
QY 2153 TTCAGAACCTGAGGCTGAAGAGGAGTGGCGCATCTCCAGCTCAGGCTCGGAGGAGCCTCTCTG 2212

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Db 2516 TGGAGACCTCGGGTGGCTGTGCGCTCACAGCTGAGGACTGCAAGGACCTTGCT 2575
Qy 2213 CAGCTCTCATAGCAATTAAGAAATTTGACAAAGGATGATCTCAGTGGCAACGGCGTTGGAT 2272
Db 2576 TTGGGCTGAGAGCCCAACAGACCTTGACCGAGCTGGACCTGAGCTTCAATGTGCTCAGG 2635
Qy 2273 TCCAGAGCATGATGCTGTTTGGAGGGCCCTGCGGCAATCCCAAGTGCAGGCTGCAGATGA 2332
Db 2636 ATGCTGGAGCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAGCTACAGCGAC 2695
Qy 2333 TTCAAGTGAAGAGTGCAGTGGAGTCCGGGCTTGTCAAGAGATGGCTTCTGTGCTCG 2392
Db 2696 TGCAGCTGGTCAAGTGTGCGCTCAGCTGACTGCTGCCAGGACCTGGCCCTCTGTGCTTA 2755
Qy 2393 GCACCAACCCACATCTGTTGAGTTGGACCTTGACAGGAAATGCACTGGAGGATTTGGGCC 2452
Db 2756 GTGCCAGCCGAGCTGAGAGCTAGACCTTGACAGCAACAACTGGATGACGTTGGCG 2815
Qy 2453 TGAGTTACTATGCCAGGAGCTGAGGACCCAGTCTGCAGACT 2495
Db 2816 TGCAGCTGCTGTGAGGGGCTCAGGCACTCCTGCTGCAAACT 2858

RESULT 6

US-08-910-731-1
; Sequence 1, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILTA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 1..1368
US-08-910-731-1
Query Match 9.6%; Score 299; DB 2; Length 1371;
Best Local Similarity 54.3%; Pred. No. 1.le-69;
Matches 605; Conservative 0; Mismatches 510; Indels 0; Gaps 0;
Qy 1971 GCACACCTGTGTGTCAGCTCAGACCAGAGAGGACCGTTCTGTGTGACGCTACAGTGA 2030
Db 63 GCTCCAGCATGATGAGTGGTTCAGGCTCGACGACTGCGGCTCACGAGGAGCACTGCAA 122
Qy 2031 ACATCTGGCAGCGCCCTGTGTGACCAATCCAAATCCTGATAGAGCTGTCTGTATCCGAAA 2090
Db 123 GGACATCGGTTCTGCCCCCTCCGGGCCAAACCCCTCCCTGACCGAGCTCTGCTCCGACCAA 182
Qy 2091 TGGCCCTGGCAGCGCGGGGTGAGCTGCTGTCTCAAGAGACTCAGACACCCCAACTGCAA 2150
Db 183 CGAGCTGGGCGATGCGCGGCTGACCTGTGTGTCAGGGGCTGCGAGAGCCCCACCTGCAA 242
Qy 2151 ACTTCAGAACTGAGGCTGAAAGAGGTGCCGCTCTCCAGCTCAGCCTGCGAGGACCTCTC 2210
Db 243 GATCCAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGAGGCGGCTGCGGGTCTCTGCC 302
Qy 2211 TGCAGCTCTCATAGCCCAATTAAGAAATTTGACAAAGATGATCTCAGTGGCAACGGCGTTGG 2270
Db 303 CAGCACGCTGCGCTCCCTGCCCCACGCTGCGGGAGCTGATCTCAGCGACAAACCCACTGGG 362
Qy 2271 ATTTCCAGGCGATGATGCTGCTTTTGCAGGGGCTGCGGCATCCCAAGTGCAGGCTGCAGAT 2330
Db 363 GGAGCGCGGCTGCGGCTGCTGTGTGAGGGGCTCTGTGACCCCCAGTGCACACCTGGAGAA 422
Qy 2331 GATTTCAGTTGAGGAAGTGTTCAGCTGGAGTCCGGGCTTGTTCAGGAGATGGCTTCTGTGCT 2390
Db 423 GCTGCACTGGAGTACTGCGGCTGACGCGCGCCAGCTGCGAGCCCTGGCTCGGTGCT 482
Qy 2391 CGGCACCAACCCACATCTGTGTGAGTTGGACCTGACAGGAAATGCATGAGAGATTTGGG 2450
Db 483 CAGGGCCACGCGGGCTTTGAAGGAGCTCAGCGTGAAGCAACCAACACATCGCGAGGCGCG 542
Qy 2451 CCTGAGGTTACTATGCCAGGAGCTGAGGACCCAGCTGCGAGACTACGAGCTTTGTGCTGCT 2510
Db 543 CGCCCGGGTGTGGGCGCAGGGTCTGCGAGACTCTGCTTGCAGCTGGAGAGCTCAGGCT 602
Qy 2511 GAAGATCTGCGGCTCACTGCTGCTGTGCTGTGAGAGCTGCGGCTCAACTCTCAGTGTGAA 2570
Db 603 GGAGAACTGGGTCTCAGCGCCAGCAACTGCMAAGACTGTGCGGAATTTGGGCTCCCA 662
Qy 2571 CCAGAGCTGAGAGAGCTGAGCCTGAGCTGAATGAGCTGGGGGACCTCGGGGTGCTGCT 2630
Db 663 GGCCTCGCTGAGGAGCTTGAACCTGGGCGAGCAACGGGCTGCGGCGACGCGGCATAGCCGA 722
Qy 2631 GCTGTGTGAGGGCTCAGGCACTCCACGTCGCAAGCTCAGACCTCGGCTGGGCACTCG 2690
Db 723 GCTGTGCCCCGGGCTCTTGAGCCCCGCTCCCGCTCAAGACCTGTGGGCTCTGGGAGTG 782
Qy 2691 CCGGCTGGGCTGTGCGGCTGTGAGGGTCTTTTGTGTGTGCTCAGGCGCAACCAACCACT 2750
Db 783 TGACATCACCGCCAGTGGCTGCAGAGACTCTGCCGTGTCTCCAGGCCAAGAGACCT 842
Qy 2751 CCGGGAGCTGGAATTTGAGTTTCAACGACTGGGAGACTGGGGCTGTGTGTGCTGGCTGA 2810
Db 843 GAAGGAGCTCAGTCTGGCGGCAACAAAGCTGGGCGAGAGGGGCGCGGCTGTGTGCGA 902
Qy 2811 GGGGCTGCACATCCCGGCTGCAGACTCCAGAACTGTGGCTGTGATAGTGTGGCTCAC 2870
Db 903 GAGCTTGTGAGCCCCGGCTGCCAGCTGGAGTCCCTGTGGGTGAAGTCTCTGACGCTCAC 962
Qy 2871 AGCCAAGGCTTGTGAGAAATCTTTACTTCACTTGGGGATCAACAGACCTTTCAGCCGACT 2930
Db 963 GCGGCGCTGCTGCCAGCAGCAGCTGACTTGTGATGCTGACCCAGCAACAGCATCTCTCGGA 1022
Qy 2931 TTACCTGACCAACAAACCGCCCTAGGGGACACAGGTGTCCGACTGCTTTTTCAGAGCGGCTGAG 2990

Db 1023 TCAGTTGAGCAGCAACAAGCTGGGTGACTCTGGCATCCAGGAGCTGTGCCAGGCCCTGAG 1082
Qy 2991 CCATCTGGCTGCAAACTCCGAGTCTCTGGTTATTGGGATGGACCTGAATAAAATGAC 3050
Db 1083 CCAGCCGGGACACACTGGGGTGCTCTGTCTTGGGAGCTGTAGGTGACCAACAGCGG 1142
Qy 3051 CCACAGTAGGTGGCAGCGCTTCGAGTAACAAAC 3085
Db 1143 CTGACAGAGCTCGCCTCGCTCTGCTGGCCAAAC 1177

RESULT 7
US-08-795-395-1
; Sequence 1, Application US/08795395
; Patent No. 5965399
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Cloning and Expression of Rat Liver and
; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,395
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
US-08-795-395-1
Query Match 9.6%; Score 299; DB 2; Length 1371;
Best Local Similarity 54.3%; Pred. No. 1.1e-69;
Matches 605; Conservative 0; Mismatches 510; Indels 0; Gaps 0;
Qy 1971 GCACACCTGTGTGTCAGCTCAGACACAGAGAGCGTTTCTGTGGAGCGCTACAGTGA 2030
Db 63 GCTCCAGATGATGAGTGTGCTGAGCTCGAGCTGGGCTCAGCGAGGAGCACTGCAA 122
Qy 2031 ACATCTGGAGCGGCCCTGTGTCACCAATCCAAACCTGATGAGCTCTCTGTACCGAA 2090
Db 123 GGACATCGGTTCTGCCCTCGGGGCCAACCCCTCCCTGACCGAGCTGTGCTCGCACCAA 182
Qy 2091 TGCCTGGGAGCGGGGGGTGAGCTGCTGTCAAGGACTCAGACACCCCACTGCAA 2150

Db 183 CGAGCTGGCGGATGCGCGGCTGCACCTGTGTCTGAGGGCCCTGCAGAGCCCACTTGCRAA 242
Qy 2151 ACTTCAGAACTGAGGTGAGGTCGCGCATCTCCAGCTCAGCTCGAGCTGGAGACCTCTC 2210
Db 243 GATCCAGAACTGAGCTGAGCAACTGCTCCCTGACCGAGGGGGCTGCGGGTCTCTGCC 302
Qy 2211 TGCAGCTCTCATAGCCAAATAAGAAATTTGACAAGATGATCTCAGTGGGCAACGGCTTGG 2270
Db 303 CAGCAGCTGGCTCCCTGCGCCAGCTGCGGAGCTGCATCTCAGCGACAAACCACTGGG 362
Qy 2271 ATTCCAGAGCATGCTGCTTTCGAGGGCTCGGCGATCCCCAGTGCAGGCTGCAGAT 2330
Db 363 GGACCGCGGCTGCGGCTGCTCTGTGAGGGGCTCTTGACCCCACTGTCACCTGGAGAA 422
Qy 2331 GATTGAGTTGAGGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2390
Db 423 GCTGAGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 482
Qy 2391 CGGCACCAACCAACATCTGTTGAGTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2450
Db 483 CAGGCCACCGCGGCTTGAAGGAGCTCAGCGTGAGCAACAACGACATCGCGGAGCGCG 542
Qy 2451 CCTGAGTTACTATGCCAGGAGCTGAGCACCCAGTCTGCAGACTACGAGCTTTGTGCT 2510
Db 543 CGCCCGGCTGCTGGGCGAGGCTGTGGCAGACTCTGCTGCTGCCAGCTGGAGAGCTCAG 602
Qy 2511 GAAAGATCTGCCGCTCTACTGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 2570
Db 603 GGAGAACTGCGTCTCTCAGCCAGCAACTGTCAAAAGACCTGTGCGGAATTTGGGCTTCCA 662
Qy 2571 CCAGAGCTGAGAGAGCTGGACCTGAGCTGAATGAGTGTGGGAGCTTGGGGTGTGCT 2630
Db 663 GGCCTGCTGAGGAGCTTGAACCTTGGGAGCAACAAGCTGGCGAGCGCGGCAATAGCG 722
Qy 2631 GCTGTGTGAGGAGCTCAGGCTATCCCACTGCAAGCTCCAGACCTTCCAGCTTGGGATCTG 2690
Db 723 GCTGTGCGCGGCTCTTGGAGCGCTTGGAGCGCTCAAGACCTTGTGCTGTGGAGTG 782
Qy 2691 CCGGCTGGGCTCTGCGGCTGTGAGGCTTCTTGTGTGTGCTTCCAGGCGCAACCAACT 2750
Db 783 TGACATCACCGCAGTGGCTGCAGAGACCTCTGCGGTGTCTTCCAGGCGCAAGAGACCT 842
Qy 2751 CCGGAGCTGGACTTGTGAGTTTCAACGACCTGGGAGACTGGGCTGTGTGCTGTGCTGA 2810
Db 843 GAAGAGCTCAGTCTGGCGGCAACAAGCTGGCGAGAGGCGCGCTCTGTGCGA 902
Qy 2811 GGGGCTGCAACATCCCGCTGAGACTCCAGAACTGTGGCTGGATAGTGTGGCTCAC 2870
Db 903 GAGCTGTGCGAGCGCGGCTGCGAGTGGAGTCCCTGTGGGTGAAGTCTCTGAGCTCAC 962
Qy 2871 AGCCAAGGCTGTGAGAACTTTTACTTTCACCTGGGGATCAACAGAGACCTTGACCGACT 2930
Db 963 GCGGCGCTGCTGCCAGACCTGAGCTGTGATGTGATGTGATGTGATGTGATGTGATGTG 1022
Qy 2931 TTACCTGACCAACAACCGCTTAGGGAGACAGGTGTCCAGTGTCCAGTGTTCAGAGGGCTGAG 2990
Db 1023 TCAGTTGAGCAGCAACAAGCTGGGTGACTCTGCGATCCAGGAGCTGTGCGAGGCTTGAG 1082
Qy 2991 CCATCTGGCTGCAAACTCCGAGTCTCTGTTTATTGGGATGAGCTGAATAAAATGAC 3050
Db 1083 CCAGCCGGGACCAACACTGCGGGTGTCTGTCTTGGGAGCTGTGAGTGACCAACAGCGG 1142
Qy 3051 CCAGTAGGTGTGAGCGCTTCGAGTAACAAAC 3085
Db 1143 CTGACAGAGCTCGCCTCGCTCTGCTGGCCAAAC 1177

RESULT 8
US-08-910-731-7
; Sequence 7, Application US/08910731
; Patent No. 5912440
; GENERAL INFORMATION:

;; APPLICANT: CHATTERJEE, DEB K.
;; APPLICANT: SHANDILYA, HARINI
;; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3934
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/910,731
;; FILING DATE: (Herewith)
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/795,395
;; FILING DATE: 04-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/794,546
;; FILING DATE: 03-FEB-1997
;; APPLICATION DATA:
;; APPLICATION NUMBER: 60/024,057
;; FILING DATE: 16-AUG-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ESMOND, ROBERT W.
;; REGISTRATION NUMBER: 32,893
;; REFERENCE/DOCKET NUMBER: 0942.3440003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1371 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: CDNA
US-08-910-731-7

Query Match 9.4%; Score 293.2; DB 2; Length 1371;
Best Local Similarity 54.2%; Pred. No. 3.8e-68;
Matches 595; Conservative 0; Mismatches 503; Indels 0; Gaps 0;
Qy 1971 GCACACGCTGTGTGAGCTCAGACGAGGAGGACCGTTCTGCTGGACGCTTACAGTGA 2030
Db 63 GCTCCAGCAGTATGAGGTGGTTCAGGCTCGACGCTGCGGCTCAGGAGGAGCACTGCA 122
Qy 2031 ACATCTGGCAGCGGCTGTGCACCAATCCAACTGATAGAGCTGTCTGTACCGAAA 2090
Db 123 GGACATCGGTTCTGCTCCGCGGCAACCCCTCCCTGACGAGCTGTGCTCCGACCAA 182
Qy 2091 TGCCTGGGACCGCGGGGTGAAGCTGTCTGTCAAGGACTCAGACACCCCACTGCAA 2150
Db 183 CGACTGGGCGATCGCGCGGTGCACTGTGCTGCTGAGGCTCGAGAGCCCACTGCAA 242
Qy 2151 ACTTCAGAACCTGAGGCTGAAGAGGTGCCGATCTCCAGCTCAGCCTGCGAGGACCTCTC 2210
Db 243 GATCCAGAAGCTCAGCTGCGAGAACTGTCTCCCTGACCGAGCGGCTGCGGGTCTGCC 302
Qy 2211 TGCAGCTCTATAGCCAAATAGAAATTTGACAAGATGATCTAGTGGCAACGCGGTGG 2270
Db 303 CAGCACGCTGCGCTCCCTGCGCCAGCTGCGGGAGCTGCATCTCAGCGACACCACTGGG 362
Qy 2271 ATTTCCAGGAGTATGCTGCTTTGCGAGGCGCTCGGCATCCCGAGCTCGAGCTGCAGAT 2330
Db 363 GGACCGCGGCTGCGGCTGTCTGTGAGGGGCTCTTGACCCCGAGTGCACCTGGAGAA 422

Qy 2331 GATTCACTTGAGGAAGTGTAGCTGAGTCCGGGGCTTGTGAGAGATGGCTTCTGTGCT 2390
Db 423 GCTGCACTTGAGTACTGCCGCTTGCAGCGGCCAGCTGCGAGCCCTTGGCTCGGTGCT 482
Qy 2391 CGGCACCAACCCACATCTGGTTGAGTTGGACCTCAGAGGAATGCACCTGGAGGATTTGGG 2450
Db 483 CAGGGCCACGCGGGCCTTGAAGGAGCTCAAGTGAAGCAACACACATCGCGAGGCCGG 542
Qy 2451 CCTGAGGTTACTATGCGCAGGAGCTGAGGACCCAGTCTGCGAGACTCGGATTTGTGCT 2510
Db 543 CGCCCGGCTGCTGGGCCAGGCTTGGCCGACTCTGCTGCGAGCTGGAGAGCTCAGGCT 602
Qy 2511 GAAGATCTGCGCCTCACTGCTGTGCTGTGAGAGTGGCCTCAACTCTCAGTGTGAA 2570
Db 603 GGAGAACTGCGGTCTCAGCGCAGCAACTGCAAGAGCTGTGCGGAAATTTGGGCTCCCA 662
Qy 2571 CCAGAGCTGAGAGAGCTGGACCTGAGCTGAATGAGTGGGGACCTCGGGGTGCTGCT 2630
Db 663 GGCCTCGCTGCGGAGCTGGCCCTGGGAGCAACAAGCTGGGTGATGTGGGCATGGCGGA 722
Qy 2631 GCTGTGAGGGGCTCAGGCAATCCAGCTCCAGCTCCAGACCTCGGGTTGGGCATCTG 2690
Db 723 GCTGTGCCAGGGCTGTCTCCACCCAGCTCCAGGCTCAGGACCTGTGGATCTGGAGTG 782
Qy 2691 CCGGCTGGGCTTGCCTGCTGTGAGGCTTTTCTGTGTGCTCCAGGCCAACCAACCT 2750
Db 783 TGGCATCACTGCCAAGGGCTCGGGGATCTGTGCCGTGCTCAGGGGCCAAGAGAGCT 842
Qy 2751 CCGGAGCTGGACTTGAATTTCAACGACCTGGGAGCTGGGGCTGTGGTTGCTGGCTGA 2810
Db 843 GAAGGAGCTCAGCTGCGCGGCAACGAGCTGGGGGATGAGGGTCCCGACTGCTGTGTGA 902
Qy 2811 GGGGCTGCAACATCCCGCTCGACACTCCAGAAACTGTGGCTGATGATGCTGGCCTCAC 2870
Db 903 GACCTCTGGAACCTGGCTGCCAGCTGGAGTCGCTGTGGTGAAGTCTTCCAGCTTCA 962
Qy 2871 AGCAAGCTTGTGAGAACTTTTACTTCACTCCCTGGGGATCAACAGACCTTTCAGCG 2930
Db 963 AGCGGCTGTGCGCCCACTTCAGCTCAGTGTGCTGGCCAGAACAGGTTTCTCTCTGAG 1022
Qy 2931 TTACTTGACCAACACCGCTAGGGGACAGGTCGAGTGTGGGATGATGATGATGATGATG 2990
Db 1023 ACAGTAAGCAACAAACAGGCTGGAGGATGCGGGCTGCGGAGCTGTGCCAGGCGCTGG 1082
Qy 2991 CCATCTGGCTGCAAACTCCGAGTCTCTGTTATTTGGGATGACCTGTAATAAATGAC 3050
Db 1083 CCAGCTGGCTCTGTGCTGCGGGTGTCTGTGGTGGCCGACTGCGCATGTGATGACAG 1142
Qy 3051 CCACAGTAGTTGGCAGC 3068
Db 1143 CTGACGAGCTGCGCGC 1160

RESULT 9

US-08-910-731-5
; Sequence 5, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

2586	GCTGACCTGAGCCTGAATGAGCTGGGGACCTCGGGGTGCTGCTGCTGTGTGAGGGCCT	2644
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2646	CAGGATCCACGTGTCAAGCTCCAGACCTCGGGTTGGGCATCTGCCGGCTGGGCTTCTGC	2705
924	GCTGGAACCTGGCTGCGAGCTGGAATGCTGTGGGTGAAGTCTTGAGCTACAGAT	983
2706	CGCCTGTGAGGGTCTTTCTGTGGTGTCTCAGGCGCAACCAACCTCGGGAGCTGGACTT	2765
984	CTGCTGCCCCCACTTCAGCTCAGTGTGCGCCAGAACAGGTTTCTCTGGAGCTACAGAT	1043
2766	GAGTTTCAACGACTGGGAGCTGGGGCTGTGTTGCTGTGGCTGAGGGCTGCAACATCC	2825
1044	AAGCAACAACAGGCTGGAGATGCGGGCTGCGGAGCTGTGCAGGGCTTGGCGCAGCC	1103
2826	CGCCTGCAGACTCCAGAAACTGTGGTGGATAGCTGTGGCTCACAGCCTCAAGGCTTGTGA	2885
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1224	CTGCTTGGGGACGCGGCTCTCTGAGTGTGGAGAGCGTCCGCGAGCGGGCTGCCT	1283
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1284	CCT 1286	

RESULT 10
 US-08-910-731-3
 ; Sequence 3, Application US/08910731
 ; Patent No. 5932440
 ; GENERAL INFORMATION:
 ; APPLICANT: CHATTERJEE, DEB K.
 ; APPLICANT: SHANDILYA, HARINI
 ; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,731
 ; FILING DATE: (Herewith)
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/795,395
 ; FILING DATE: 04-FEB-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/794,546
 ; FILING DATE: 03-FEB-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60/024,057
 ; FILING DATE: 16-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ESMOND, ROBERT W.
 ; REGISTRATION NUMBER: 32,893
 ; REFERENCE/DOCKET NUMBER: 0942.3440003
 ; TELECOMMUNICATION INFORMATION:


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; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 395:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPLBL02
; CLONE: 153338
; US-09-023-655-395

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Best Local Similarity 61.2%; Pred. No. 3.4e-12;
Matches 167; Conservative 0; Mismatches 104; Indels 2; Gaps 2;

Qy 2708 CCTGTGAGGGTCTTTCTGTGTGCTCCAGGCCAACCAACT-CCGGGAGCTGGACTTG 2766
Db 2 CCTGCTCGACATCTCTGTGTCTCAGCAGCACAGAGCTGGTTGGAGCTGGACTG 61
Qy 2767 AGTTTCAACGACTGGGAGACTGGGGCTGTGGTGTGCTGGCTGAGGGCTGCAACATCCC 2826
Db 62 AGTGACAACGCCCTCGGTGACTTCGGAATCAGACTTCTGTGTGTGGGACTGAAGCACCTG 121
Qy 2827 GCCTGCGAGCTCCAGAACTGTGGCTGATGCTGCTCAGCAGCCAGCAAGCTTGTGAG 2886
Db 122 TTGTGCAATCGAAGAAGCTCTGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
Qy 2887 AATCTTTACTTTCACCTCGGGATCAACGACACCTTTGACC-GACCTTTTACCTGACCAACAA 2945
Db 182 GATCTTNCATCAGTATTGAGCACCAGCCATTCCTTGACAGACCTCTATGTGGGGAGAA 241
Qy 2946 CGCCTTAGGGACACAGGTGCCGACTGCTTTTG 2978
Db 242 TGCCTTGGGAGACTCAGGAGTCGCAATTTATG 274

RESULT 14
US-09-016-434-1011
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; Sequence 1011, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
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; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1011:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT04
; CLONE: 927003
; US-09-016-434-1011

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Best Local Similarity 53.3%; Pred. No. 1.7e-10;
Matches 218; Conservative 0; Mismatches 186; Indels 5; Gaps 3;

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Db 63 CNCNCTGTTCTTGTGCTGCTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 122
Qy 1173 GGAGGTGGGGGCTGTGTGAGACAGAGCTCC-AGGACCACTGCTGAGTGTACATGTCT 1231
Db 123 GGAGCTCGTCCGGACCTGTCCGCGACCTCAAGGACCACTGCTGAGTGTACCTGCTTT 182
Qy 1232 ACTGTGAGTCTGTGATCAACCCAGCCGGGGCCCCCGCTCCAGCCCCCACCACC 1291
Db 183 TCATACACANNNTTCTGAGCTCCGCTCCGTCGACCGGCCCGCTGTCAGGGCGACC 242
Qy 1292 AGAGAGGTGTGCTCTCTGGCGCAGATGGGCTCTGGAATCAGAAAAATCCTATTGAGG 1351
Db 243 TGGCCTATCTGTGCGGCTGCGCGCGGCGGCGCTCTCGGACGCGAGGGCGGCGGCGGCGG 302
Qy 1352 AGCAGGACTTCCGGAAGCAGCGGCT---AGACGGGGGAAGAGCTCTCTGCTTCTCTCAACA 1408
Db 303 AGAAGGAACCTGGAGCACTGGAGCTTGTGCTGCTCCAAAGTGACAGCTGTTTCTCANCA 362
Qy 1409 TGAACATCTTCCAGAGGACATCACTGTGAGAGGTACTACAGCTTCATCCACTTGATT 1468
Db 363 AAAAGGACTGCCGGGCTGTCTGGAACAGAGGTCACCTACCACTTCATCGGACGAGCT 422
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1420 CGCACCGAGTTCAACCTCAAGGGCTTCTCTGAACAGGGCATCGAGCTGTCTGAGGAAG 1479
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1480 CGCCATCATGAGCCCGGGGTGGCGGACCGCTCATCGCCCTGTCTCCAGAGACCTCAGCC 1539
1108 CTCTTTACCAATGTGCTTTCGTCCCTCGTGGTGTGGTGTGTGTACTCTGCTTCCAGCAG 1167
1540 CTGACGGTTTGTGCCACCTGCTGTCTTCTCATGGATGCTGTCCAAATGCCACAGGAA 1599
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1469 TCAGGAATT-CTTTCAGCATGTACTATATCTCGACGAGGGGAGG 1516
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RESULT 15
US-09-949-016-3209
; Sequence 3209, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3209
; LENGTH: 4485
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3209

Query Match 2.2%; Score 68.2; DB 4; Length 4485;
Best Local Similarity 48.1%; Pred. No. 1.3e-07;
Matches 364; Conservative 0; Mismatches 368; Indels 25; Gaps 5;

Qy 461 GGGGACAGCGAGGACCGCGGAGCCACCGGACCGGTGTCATGCAAGGCGGCGAGGG 579
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Qy 520 GAGCCAGAGGAGGAGCGCGGAGCCACCGGACCGGTGTCATGCAAGGCGGCGAGGG 579
Db 952 AGCACCCCTGGCCACCTCAATGACGATCGGACACTGTGTGGTGGTGGGCGGCG 1011
Qy 580 ATAGGCAAGTCATGCTGGGACACAGGTGATGTGACTGGGCGGAGCGGAGCTCTTC 639
Db 1012 AGTGGCAAGAGCACGCTCTGCGAGCGGCTGCACTTGTGTGGGTGCGAGGGCAAGACTTC 1071
Qy 640 CAAGGCAAGTTGATTATCTCTTCTACATCAACTGCGGAGAGATGAACAGAGTGCCACG 699
Db 1072 CAGG---AATTTCTTTTGTCTTCCANTTACGTCGCGGAGCTGCACTGATGCGCCAAA 1128
Qy 700 GAATGAGCATGAAGACCTCATCTTCAAGCTGCTGGCCTGAGCCCGGCGCCTCTCCAG 759
Db 1129 CCACCTCTGTGGGACTCTACTCTTGAGCACTGCTGTGGCCTGATGTTGGTCAAGAA 1188
Qy 760 GAGCTCATCGAGTTCCC-----GAGCGCTCTTTTCATCATCGACGGCTTC 807
Db 1189 GACATCTTCCAGTTACTCTTGGACACCCCTGACCGATCGTGAACGCCACTG-----CTCCCGGACCGAC 1248
Qy 808 GATGAGCTCAAGCTTCTTTCCAGCATCTCTCAGGAGCCCTGTGTGCTCTGTGGGAGGAG 867
Db 1249 GACGAGTTCAAGTTCAGGTTACGGATCGTGAACGCCACTG-----CTCCCGGACCGAC 1302
Qy 868 AAACGGCCCAACGAGTGTCTTTAAAGCTTAATTCGAAGAAGCTGCTCCCTGAGCTA 927
Db 1303 CCCACCTCTGTCCAGACCCCTGCTTCAACCTTCTGAGGGCAACCTGCTGAAGATGCC 1362
Qy 928 TCTTTGCTCATACCAACAGCGGCGGCTTTGGAGAAGCTCCACCGTCTGCTGGAGCAC 987
Db 1363 CGCAAGGTGTGACCGCGCTGCGGCGGCTGTGTCGGCTTCTCAG---GAAGTACATC 1419
Qy 988 CCCAGGCAATGGAGATCTCTGGGCTTCTGTGAGGCGAAGAGGAGATATCTTCTACAG 1047

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Searched: 4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

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- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
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- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3108	100.0	3108	17	US-10-407-866-23
3	3108	100.0	3108	17	US-10-781-294-23
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5	2997.8	96.5	3186	14	US-10-066-521-17
6	2929	94.2	3218	17	US-10-407-866-67
7	2644.2	85.1	3466	17	US-10-108-260A-718
8	1705.4	54.9	1800	17	US-10-162-335-21
9	1681.8	54.1	2158	18	US-10-467-397-19
c 10	1680	54.1	1704	16	US-10-029-386-24660
11	1616	52.0	4931	15	US-10-028-374-1
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					Sequence 23, Appl
					Sequence 23, Appl
					Sequence 17, Appl
					Sequence 17, Appl
					Sequence 67, Appl
					Sequence 718, Appl
					Sequence 21, Appl
					Sequence 19, Appl
					Sequence 24660, A
					Sequence 1, Appl

12	1616	52.0	4931	16	US-10-183-770-1	Sequence 1, Appl
13	1394.8	44.9	1683	17	US-10-162-335-23	Sequence 23, Appl
14	947.6	30.5	2682	9	US-09-799-983-1	Sequence 1, Appl
15	800.4	25.8	3102	13	US-10-127-516-6	Sequence 6, Appl
16	800.4	25.8	3102	13	US-10-027-629-6	Sequence 6, Appl
17	800.4	25.8	3102	16	US-10-132-967-6	Sequence 6, Appl
18	800.4	25.8	3857	13	US-10-127-516-4	Sequence 4, Appl
19	800.4	25.8	3857	13	US-10-027-629-4	Sequence 4, Appl
20	800.4	25.8	3857	16	US-10-132-967-4	Sequence 4, Appl
21	800	25.7	4193	17	US-10-264-958B-21	Sequence 21, Appl
22	691	22.2	2511	9	US-09-799-983-5	Sequence 5, Appl
23	639	20.6	2524	10	US-09-965-621-58	Sequence 58, Appl
24	639	20.6	2524	17	US-10-407-866-58	Sequence 58, Appl
25	639	20.6	2524	18	US-10-781-294-58	Sequence 58, Appl
26	595.6	19.2	2494	9	US-09-799-983-3	Sequence 3, Appl
c 27	509	16.4	509	16	US-10-029-386-10957	Sequence 10957, A
28	475.4	15.3	3521	18	US-10-794-342-2	Sequence 2, Appl
29	453.4	14.6	487	10	US-09-918-995-23437	Sequence 23437, A
30	435.6	14.0	2775	17	US-10-357-820-51	Sequence 51, Appl
31	404.4	13.0	4035	14	US-10-124-498-5	Sequence 5, Appl
32	404.4	13.0	4035	14	US-10-066-521-5	Sequence 5, Appl
33	402.8	13.0	3226	17	US-10-092-900A-347	Sequence 347, App
34	402.8	13.0	3489	17	US-10-416-642-3	Sequence 3, Appl
35	402.8	13.0	3830	15	US-10-216-645-3	Sequence 3, Appl
36	402.8	13.0	3926	15	US-10-216-645-1	Sequence 1, Appl
37	401.2	12.9	3885	18	US-10-860-761-3	Sequence 3, Appl
38	401.2	12.9	3900	17	US-10-399-443-23	Sequence 23, Appl
39	401.2	12.9	3900	17	US-10-677-943-23	Sequence 23, Appl
40	398	12.8	4287	9	US-09-996-617-5	Sequence 5, Appl
41	398	12.8	4287	9	US-09-931-071-5	Sequence 5, Appl
42	398	12.8	4422	9	US-09-388-221-1	Sequence 1, Appl
43	398	12.8	4422	18	US-10-828-920-1	Sequence 1, Appl
44	398	12.8	4556	9	US-09-388-221-9	Sequence 9, Appl
45	398	12.8	4556	18	US-10-828-920-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-965-621-23
; Sequence 23, Application US/09965621
; Publication No. US20030077699A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Ioredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/09/965,621
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3105)
US-09-965-621-23

Query Match 100.0%; Score 3108; DB 10; Length 3108;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	121	GCACAGATCCCTCGGGAGCATGAGAAAGCCGGTCCCTCGGAAATGGCCACAGCTGCTC	180
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QY	181	ATCACCCACTTCGGGCCAGAGAGGCCCTGGAGGTTGGCTCTCAGCACCTTTGAGCGGATA	240
Db	181	ATCACCCACTTCGGGCCAGAGAGGCCCTGGAGGTTGGCTCTCAGCACCTTTGAGCGGATA	240
QY	241	AACAGGAAGCACTGTGGGAGAGGACAGAGAGGACCTGTGGAGGATCCCCAGGAA	300
Db	241	AACAGGAAGCACTGTGGGAGAGGACAGAGAGGACCTGTGGAGGATCCCCAGGAA	300
QY	301	ACCTACAGGACATATGTCGCGCAGGAAATTCGGGCTCATGGAAGACCGCAATGCGCGCTA	360
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QY	361	GGGGAATGTGTAACTCAGCCACCGGTACACCGGCTCCCTGCTGGTGAAGGACACTCA	420
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QY	421	AAACCCATGAGCTCAGCAGCAGCTTCTGGACACAGGCGCGGACACGCGAGGACCGTG	480
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QY	541	GAGCCACCGGCAACCTGTGTCATGAAGCGCGGAGGATAGGCAAGTCCATGCTGGCA	600
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QY	601	CACAAGGTGATGTGGACTGGGCGGACGGGAAGCTTTCCAAAGGAGATTTGATTATCTC	660
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Db	781	CGCCTCTCTTTTCATCATCAGCGGCTTCGATGAGCTCAAGCCTCTTTCACCATCCTCAG	840
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Db	841	GGACCTCTGGTCTGCTGGGAGAGAAACGGCCACCGAGTGTCTTTAACAGCTTA	900
QY	901	ATTTCGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCAACACAGCGGCCAGGCTTGG	960
Db	901	ATTTCGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCAACACAGCGGCCAGGCTTGG	960
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Db	961	GAGAGCTCCACCGTCTGCTGGAGACCCAGGACATGTGGATCTCTGGGCTTCTCTGAG	1020
QY	1021	GCAGAAAGGAAGAATACTTCTACAAGTATTTCCACAATGAGAGCGCGGCCAAGTC	1080
Db	1021	GCAGAAAGGAAGAATACTTCTACAAGTATTTCCACAATGAGAGCGCGGCCAAGTC	1080
QY	1081	TTCAATTACGTAGGGACAAAGAGCTCTCTTCAACCATGTGCTTCGTCGCCCTGGTGTC	1140

Qy 3001 TGCAGGCTCCGAGTCTCTGTTATTTGGGATGGAACCTTAAATGACCCACAGTAGG 3060
Db 3001 TGCAGGCTCCGAGTCTCTGTTATTTGGGATGGAACCTTAAATGACCCACAGTAGG 3060
Qy 3061 TTGGCAGGCTTCGAGTAACAAAACCTTATTTGGACATTTGCTGCTGA 3108
Db 3061 TTGGCAGGCTTCGAGTAACAAAACCTTATTTGGACATTTGCTGCTGA 3108

RESULT 3
US-10-781-294-23
; Sequence 23, Application US/10781294
; Publication No. US20040142374A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
; TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/10/781,294
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3105)
US-10-781-294-23

Query Match 100.0%; Score 3108; DB 18; Length 3108;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTACGAACCGCAGGACGAGCGCTCTGTCGCTGTCCACCTACTTGGAGAATC 60
Db 1 ATGCTACGAACCGCAGGACGAGCGCTCTGTCGCTGTCCACCTACTTGGAGAATC 60
Qy 61 GAGGCTGTGGAACCTCAAGATTATACCTGGGAGCCGCGACAGAGCTGGAGAA 120
Db 61 GAGGCTGTGGAACCTCAAGATTATACCTGGGAGCCGCGACAGAGCTGGAGAA 120
Qy 121 GCGAAGATCCCTGGGAGCATGAGAGCCGGTCCCTGGAAATGGCCAGCTGCTC 180
Db 121 GCGAAGATCCCTGGGAGCATGAGAGCCGGTCCCTGGAAATGGCCAGCTGCTC 180
Qy 181 ATACCCCACTTCGCGGACAGAGAGCGCTGGAGGTTGGCTCTCAGCACCTTTGAGCGGATA 240
Db 181 ATACCCCACTTCGCGGACAGAGAGCGCTGGAGGTTGGCTCTCAGCACCTTTGAGCGGATA 240
Qy 241 AACAGGAGGACCTGTGGGAGAGGACAGAGAGGACCTGGTGGAGGATCCCGAGGAA 300
Db 241 AACAGGAGGACCTGTGGGAGAGGACAGAGAGGACCTGGTGGAGGATCCCGAGGAA 300
Qy 301 ACCTACAGGAGCTATGTCCGAGAGAAATTCGGCTCATGGAAGACCGCAATGGCGGCTTA 360
Db 301 ACCTACAGGAGCTATGTCCGAGAGAAATTCGGCTCATGGAAGACCGCAATGGCGGCTTA 360
Qy 361 GGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCTGCTGGTGGAGGAGCACTCA 420
Db 361 GGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCTGCTGGTGGAGGAGCACTCA 420

Qy 421 AACCCCATGAGGTCAGAGTCTTCTGACACACAGCCCGGGGACACGCGAGACCGGTG 480
Db 421 AACCCCATGAGGTCAGAGTCTTCTGACACACAGCCCGGGGACACGCGAGACCGGTG 480
Qy 481 GGACACAGGCTAGCCCCATCAAGATAGACACCTCTTTGAGCCAGAGGAGGCGCCCC 540
Db 481 GGACACAGGCTAGCCCCATCAAGATAGACACCTCTTTGAGCCAGAGGAGGCGCCCC 540
Qy 541 GAGCCACCGCGCACCGTGGTTCATGCAAGGCGCGCAGGAGTAGGCAAGTCCATCTGGCA 600
Db 541 GAGCCACCGCGCACCGTGGTTCATGCAAGGCGCGCAGGAGTAGGCAAGTCCATCTGGCA 600
Qy 601 CACAAGGTGATGTGAGTCTGGGCGGACGGAAGCTTTTCCAAAGCAGATTTGATATCTC 660
Db 601 CACAAGGTGATGTGAGTCTGGGCGGACGGAAGCTTTTCCAAAGCAGATTTGATATCTC 660
Qy 661 TTCTTACATCAACTGCAGGGAGATGAACAGAGTGCACGGAATGCACATGCACAGATCTC 720
Db 661 TTCTTACATCAACTGCAGGGAGATGAACAGAGTGCACGGAATGCACATGCACAGATCTC 720
Qy 721 ATCTTACAGTCTGCTGGCTGAGCCCGCGCTCTCCAGGAGCTCATCCGAGTTCCTCGAG 780
Db 721 ATCTTACAGTCTGCTGGCTGAGCCCGCGCTCTCCAGGAGCTCATCCGAGTTCCTCGAG 780
Qy 781 CGCCTCCTTTTTCATCATCGAGCGCTTCGATGAGCTCAAGCTCTTTTCCACGATCTCTCAG 840
Db 781 CGCCTCCTTTTTCATCATCGAGCGCTTCGATGAGCTCAAGCTCTTTTCCACGATCTCTCAG 840
Qy 841 GGAACCTGTGCTCTGCTGGGAGGAGAAACGCGCCACGAGCTGCTTTTAAACAGCTTA 900
Db 841 GGAACCTGTGCTCTGCTGGGAGGAGAAACGCGCCACGAGCTGCTTTTAAACAGCTTA 900
Qy 901 ATTCGGAAGAGTGTCTCCCTGAGCTATCTTTGTCTATCAACACACGCGCCACCGCTTTG 960
Db 901 ATTCGGAAGAGTGTCTCCCTGAGCTATCTTTGTCTATCAACACACGCGCCACCGCTTTG 960
Qy 961 GAGAAGCTCCACCGTCTGCTGGAGCACCCAGGAGCTGAGAGTCTTGGGCTCTCTGAG 1020
Db 961 GAGAAGCTCCACCGTCTGCTGGAGCACCCAGGAGCTGAGAGTCTTGGGCTCTCTGAG 1020
Qy 1021 GCAGAGGAGGAGTACTTCTACAGTATTTCCACATTCAGAGTCTGAGTGCAGGAGCGGCGCAAGTC 1080
Db 1021 GCAGAGGAGGAGTACTTCTACAGTATTTCCACATTCAGAGTCTGAGTGCAGGAGCGGCGCAAGTC 1080
Qy 1081 TTCAATTTACGTGAGGAGCAACGAGCTCTCTTCAACATGTCTTCTGCTCCCTGGTGTGC 1140
Db 1081 TTCAATTTACGTGAGGAGCAACGAGCTCTCTTCAACATGTCTTCTGCTCCCTGGTGTGC 1140
Qy 1141 TGGGTGTGTGTACCTGCTCCAGCAGCAGCTGGAGGGTGGGGGCTGTTGAGACAGACG 1200
Db 1141 TGGGTGTGTGTACCTGCTCCAGCAGCAGCTGGAGGGTGGGGGCTGTTGAGACAGACG 1200
Qy 1201 TCCAGGACCACTGAGGTGATACGTCTTCTGCTGAGTCTGATGCAACCCCAAGCG 1260
Db 1201 TCCAGGACCACTGAGGTGATACGTCTTCTGCTGAGTCTGATGCAACCCCAAGCG 1260
Qy 1261 GGGGCCCGCGCTCTCAGACCCCAACCAACAGAGGGTGTGCTCTTTGGCGGAGAT 1320
Db 1261 GGGGCCCGCGCTCTCAGACCCCAACCAACAGAGGGTGTGCTCTTTGGCGGAGAT 1320
Qy 1321 GGGCTCTGGAATCAGAAAATCTTATTTGAGGAGCAGGACCTCCGGAAGCAGCGCTGAGC 1380
Db 1321 GGGCTCTGGAATCAGAAAATCTTATTTGAGGAGCAGGACCTCCGGAAGCAGCGCTGAGC 1380
Qy 1381 GGGGAGACCTCTGCTCTTCTCAACATGAAATCTTCCAGAGGAGGATCACTGAG 1440
Db 1381 GGGGAGACCTCTGCTCTTCTCAACATGAAATCTTCCAGAGGAGGATCACTGAG 1440
Qy 1441 AGGTACTTACAGCTTCTATCCAGTGTTCAGGAATCTTTTGGAGCTATGTACTATATC 1500
Db 1441 AGGTACTTACAGCTTCTATCCAGTGTTCAGGAATCTTTTGGAGCTATGTACTATATC 1500
Qy 1501 CTGGAACGAGGGGAGGGCGGCGGAGCCAGACGAGGAGCTGAGCAGGCTGTTGACCGAG 1560

Db	1501	CTGCA CGAGGGGAGGGCGGGCGAGCCAGAGCACTGACAGGCTGTTACCGAG	1560
Qy	1561	TAGCGCTTTTCTGAAGGAGCTTCTTGGCACTACACAGCGCTTCTGTTTGGACTCCTG	1620
Db	1561	TACGCGCTTTTCTGAAGGAGCTTCTTGGCACTACACAGCGCTTCTGTTTGGACTCCTG	1620
Qy	1621	AACGAGGAGACCAAGGAGCCACTTGGAGAAAGTCTCTGCTGGAAGTCTCGCGGCAATC	1680
Db	1621	AA CGAGGAGACCAAGGAGCCACTTGGAGAAAGTCTCTGCTGGAAGTCTCGCGGCAATC	1680
Qy	1681	AAGATGACCTGTTGCAATGGATCCTGAGCAAGCTCAGAGCGCGCTCCACCCCTGCAG	1740
Db	1681	AAGATGACCTGTTGCAATGGATCCTGAGCAAGCTCAGAGCGCGCTCCACCCCTGCAG	1740
Qy	1741	CAGGGCTCTTGGAGTTCTTACGCTCTGTACGAGATCCAGAGAGGAGTGTATCCAG	1800
Db	1741	CAGGGCTCTTGGAGTTCTTACGCTCTGTGTACGAGATCCAGAGAGGAGTGTATCCAG	1800
Qy	1801	CAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAACATTTGCCCTCAAGATGAGCAC	1860
Db	1801	CAGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAACATTTGCCCTCAAGATGAGCAC	1860
Qy	1861	ATGCTCTCTGCTTCTGTGAAGCGCTGACAGAGCGCCAGGTGCTGCACTTGTATGGC	1920
Db	1861	ATGCTCTCTGCTTCTGTGAAGCGCTGACAGAGCGCCAGGTGCTGCACTTGTATGGC	1920
Qy	1921	GCCACCTACAGCGCGGAGCGGGAAGACCGCGCAGGTGCTCCGAGGAGCGACACGCTG	1980
Db	1921	GCCACCTTACAGCGCGGAGCGGGAAGACCGCGCAGGTGCTCCGAGGAGCGACACGCTG	1980
Qy	1981	TTGGTGCACTGTCAGACCAAGAGAGACCGTTCTGCTGGAAGCGCTACAGTGAACATCTGGCA	2040
Db	1981	TTGGTGCACTGTCAGACCAAGAGAGACCGTTCTGCTGGAAGCGCTACAGTGAACATCTGGCA	2040
Qy	2041	CGGGCTCTGACCAATCCAAACCTCATAGAGCTGTCTGTACCGAAATGCCCTGGGC	2100
Db	2041	CGGGCTCTGTCACCAATCCAAACCTCATAGAGCTGTCTGTACCGAAATGCCCTGGGC	2100
Qy	2101	AGCCGGGGGTGAAGTCTCTGTCAAGGACTCAGACACCCCAACTGCAAAATTGAGAAC	2160
Db	2101	AGCCGGGGGTGAAGTCTCTGTCAAGGACTCAGACACCCCAACTGCAAAATTGAGAAC	2160
Qy	2161	CTGAGGCTGAAGAGTGCCGATCTCCAGTCAAGCTGCGAGAGCTCTCTGAGCTCTC	2220
Db	2161	CTGAGGCTGAAGAGTGCCGATCTCCAGTCAAGCTGCGAGAGCTCTCTGAGCTCTC	2220
Qy	2221	ATAGCCAAATGAATTTGCAAGGATGGATCTCAGTGGCAACGGCGTTGATTCACGGC	2280
Db	2221	ATAGCCAAATGAATTTGCAAGGATGGATCTCAGTGGCAACGGCGTTGATTCACGGC	2280
Qy	2281	ATGATGCTGCTTTGCGAGGGCTGCGGATCCCAAGTCAAGCTGAGATGATTCAGTTG	2340
Db	2281	ATGATGCTGCTTTGCGAGGGCTGCGGATCCCAAGTCAAGCTGAGATGATTCAGTTG	2340
Qy	2341	AGGAAGTGTACAGTGGAGTCCGGGCTTGTACAGAGATGGCTTCTGTGCTCGGCACCAAC	2400
Db	2341	AGGAAGTGTACAGTGGAGTCCGGGCTTGTACAGAGATGGCTTCTGTGCTCGGCACCAAC	2400
Qy	2401	CCACATCTGTTTGAATGGACCTGACAGGAAATGCATGAGGAAATTTGGGCTGAGGTTA	2460
Db	2401	CCACATCTGTTTGAATGGACCTGACAGGAAATGCATGAGGAAATTTGGGCTGAGGTTA	2460
Qy	2461	CTATGCCAGGACTGAGGACCCAGCTCTGCAGACTACCGACTTTGTGGCTGAAGATCTGC	2520
Db	2461	CTATGCCAGGACTGAGGACCCAGCTCTGCAGACTACCGACTTTGTGGCTGAAGATCTGC	2520
Qy	2521	CGCCTCACTGCTGCTGCAAGCTGAGGCTGAGGCTCAACTCTCAGTGTGAACACGAGCCTG	2580
Db	2521	CGCCTCACTGCTGCTGCAAGCTGAGGCTGAGGCTCAACTCTCAGTGTGAACACGAGCCTG	2580
Qy	2581	AGAGAGCTGGAACCTGAGCCCTGAATAGCTGGGGGACCTCGGGGTCTGCTGCTGTGAG	2640

Db	2581	AGAGAGCTGGAACCTGAGCCCTGAATGAGCTGGGGGACCTCGGGGTGCTGCTGCTGTGAG	2640
Qy	2641	GGCCTCAGAGCATCCCAAGCTGCAGACCCCTGCGGTTGGGCATCTGCCGCTGGGC	2700
Db	2641	GGCCTCAGGCATCCCAAGCTGCAGACCCCTGCGGTTGGGCATCTGCCGCTGGGC	2700
Qy	2701	TCTGCCCCCTGTGAGGGTCTTTCTGTGTGTCTCAGGCCAACCAACTCCGGGAGCTG	2760
Db	2701	TCTGCCCCCTGTGAGGGTCTTTCTGTGTGTCTCAGGCCAACCAACTCCGGGAGCTG	2760
Qy	2761	GACTCAGTTTCAACGACCTGGGAGACTGGGGCTGTGTTGCTGTGCTGAGGGGTGCAA	2820
Db	2761	GACTTGAGTTTCAACGACTGGGAGACTGGGGCTGTGTTGCTGTGCTGAGGGGTGCAA	2820
Qy	2821	CATCCGCCCTGCAGACTGCAGAAACTGTGGCTGGATAGCTGTGGCTCACAGCCAGGCT	2880
Db	2821	CATCCGCCCTGCAGACTGCAGAAACTGTGGCTGGATAGCTGTGGCTCACAGCCAGGCT	2880
Qy	2881	TGTGAGAACTTTTACTTTCACCTTGGGATCAACAGACCTTGACCGACCTTTACCTGACC	2940
Db	2881	TGTGAGAACTTTTACTTTCACCTTGGGATCAACAGACCTTGACCGACCTTTACCTGACC	2940
Qy	2941	AACAAACCCCTTAGGGACAAGGTGTCGACTCTTTGCAAGCGGTGAGCCATCTGGC	3000
Db	2941	AACAAACCCCTTAGGGACAAGGTGTCGACTCTTTGCAAGCGGTGAGCCATCTGGC	3000
Qy	3001	TGCAAACTCCGAGTCCTCTGGTTATTTTGGGATGGAACCTGAAATAAAATGACCAAGTAGG	3060
Db	3001	TGCAAACTCCGAGTCCTCTGGTTATTTTGGGATGGAACCTGAAATAAAATGACCAAGTAGG	3060
Qy	3061	TTGGCAGCGCTTCAGTAACAAACCTTATTGGACATTTGGCTGCTGA	3108
Db	3061	TTGGCAGCGCTTCAGTAACAAACCTTATTGGACATTTGGCTGCTGA	3108

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RESULT 4
US-10-124-498-17
; sequence 17, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weihe
; APPLICANT: Blacher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TYPE OF INVENTION: PROTEIN FAMILY AND US
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (3183)
US-10-124-498-17

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Query Match	96.5%	Score 2997.8;	DB 14;	Length 3186;
Best Local Similarity	97.3%;	Pred. No. 0;		
Matches 3103; Conservative	0;	Mismatches	2;	Indels 84; Gaps 2;

Qy 1 ATGCTACGAACCGCAGGACGGACGGCCCTCTGTGCGCTTCCACCTACTTGGAGAACTC 60

db 1 ATGCTACGAACCGCAGGACGGACGGCCCTCTGTGCGCTTCCACCTACTTGGAGAACTC 60

2218 CCCAACTGCAAACTTCAGAACTGAGGCTGAAGAGTGCCGATCTCCAGCTCAGCCTGC 2277
Db
2200 GAGGACCTCTCAGCTCTCATAGCAATAGATTTGACAGGATGATCTCAGTGGC 2259
Qy
2278 GAGGACCTCTCAGCTCTCATAGCAATAGATTTGACAGGATGATCTCAGTGGC 2337
Db
2260 AACGGCTTGATTTCCAGGATGATGCTGCTTTGCGAGGCTGCGGATCCCCAGTGC 2319
Qy
2338 AACGGCTTGATTTCCAGGATGATGCTGCTTTGCGAGGCTGCGGATCCCCAGTGC 2397
Db
2320 AGGCTGAGATGATTTGAGGATGATGCTGCTTTGCGAGGCTGCGGATCCCCAGTGC 2379
Qy
2398 AGGCTGAGATGATTTGAGGATGATGCTGCTTTGCGAGGCTGCGGATCCCCAGTGC 2457
Db
2380 GCTTCTGCTGCTGCGACCAACCCACATCTGTTGAGTTGACCTGACAGAAATGCATG 2439
Qy
2458 GCTTCTGCTGCTGCGACCAACCCACATCTGTTGAGTTGACCTGACAGAAATGCATG 2517
Db
2440 GAGGATTTGGGCTGAGGTTACTATGCGAGGATGAGGACCCAGTCTGCAGACTACGG 2499
Qy
2518 GAGGATTTGGGCTGAGGTTACTATGCGAGGATGAGGACCCAGTCTGCAGACTACGG 2577
Db
2500 ACTTTGCTGAGATGCTGCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2559
Qy
2578 ACTTTGCTGAGATGCTGCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2637
Db
2560 CTCAGTGTAAACAGAGCTGAGAGAGCTGAGACCTGAGCCTGAAATGAGCTGGGGACCTC 2619
Qy
2638 CTCAGTGTAAACAGAGCTGAGAGAGCTGAGACCTGAGCCTGAAATGAGCTGGGGACCTC 2697
Db
2620 GGGTGTCTGCTGCTGAGGCTCAGGATCCAGCTGCAAGCTCCAGACCTGCGG 2679
Qy
2698 GGGTGTCTGCTGAGGCTCAGGATCCAGCTGCAAGCTCCAGACCTGCGG 2757
Db
2680 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2739
Qy
2758 TTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2817
Db
2740 AACCAAACTCCGGGAGCTGAGCTTGAATTTCAACGACCTGGGAGCTGGGCTGCTG 2799
Qy
2818 AACCAAACTCCGGGAGCTGAGCTTGAATTTCAACGACCTGGGAGCTGGGCTGCTG 2877
Db
2800 TTGCTGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCT 2859
Qy
2878 TTGCTGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCT 2937
Db
2860 TTGCTGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCT 2919
Qy
2938 TTGCTGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCT 2997
Db
2920 TTGCTGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCT 2979
Qy
2998 TTGCTGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCT 3057
Db
2980 AACGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCTGCT 3039
Qy
3058 AACGGCTGAGGCTGCAACATCCGCTGCTGAGGCTCTTTCTGCTGCTGCTGCTGCTGCT 3117
Db
3040 AATAAAATGACCAAGTGGGAGGCTTCCAGTAAACAACTTTATTTGACATTT 3099
Qy
3118 AATAAAATGACCAAGTGGGAGGCTTCCAGTAAACAACTTTATTTGACATTT 3177
Db
3100 GGCTGCTGA 3108
Qy
3178 GGCTGCTGA 3186
Db

RESULT 5
US-10-066-521-17
; Sequence 17, Application US/10066521
; Publication No. US2003002775A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John

APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 07334-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3186
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3183)
US-10-066-521-17

Query Match 96.5%; Score 2997.8; DB 14; Length 3186;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 3103; Conservative 0; Mismatches 2; Indels 84; Gaps 2;

QY 1 ATGCTACGAACCCGAGGAGGAGGAGGCTCTGTCGCTGCTCCACTTACTTGGAAAGAACTC 60
Db 1 ATGCTACGAACCCGAGGAGGAGGAGGCTCTGTCGCTGCTCCACTTACTTGGAAAGAACTC 60
QY 61 GAGGCTGTGGAACCTGAAGAAGTTCAAGTTATACCTGGGAGCCGAGACAGAGCTGGAGAA 120
Db 61 GAGGCTGTGGAACCTGAAGAAGTTCAAGTTATACCTGGGAGCCGAGACAGAGCTGGAGAA 120
QY 121 GCGAGATCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
Db 121 GCGAGATCCCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 ATCAACCACTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
Db 181 ATCAACCACTTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 AACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 288
Db 241 AACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 289 ----- 288
Db 301 GGTGGCCGCTCTCACTTGGGAACCAAGTCAACATGCTTCTGGAAGTCTCTCTTGTCACT 360
QY 289 -----GATCCCGAGGAACCTACAGGAGCTATGTCGAGGAGAAATTCGGGCTCATG 339
Db 361 CCAAGAAAGATCCCGAGGAACCTACAGGAGCTATGTCGAGGAGAAATTCGGGCTCATG 420
QY 340 GAGAGCGCAATCCGCGCTTAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399
Db 421 GAGAGCGCAATCCGCGCTTAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 400 CTGCTGTGTAAGAGGAGCACTCAAAACCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459
Db 481 CTGCTGTGTAAGAGGAGCACTCAAAACCCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 460 CGGGGACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 519
Db 541 CGGGGACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 520 GAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 579
Db 601 GAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 580 ATAGGCAAGTCCATGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 639
Db 661 ATAGGCAAGTCCATGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720

Qy	610	CAAGCAGATTGATTAATCTCTTCTACATCAACTGCAGGAGATGAACACAGAGTGCCACG	699	Qy	1720	AGCGACGGCTCCACCCCTGCAGCAGGGCTCTCTTGAGTCTTTCAGCTGCTTGTACAGATC	1779
Db	721	CAAGCAGATTGATTAATCTCTTCTACATCAACTGCAGGAGATGAACACAGAGTGCCACG	780	Db	1801	AGCGACGGCTCCACCCCTGCAGCAGGGCTCTCTTGAGTCTTTCAGCTGCTTGTACAGATC	1860
Qy	700	GAATGCAGCATGCAAGACCTCATCTTTCAGCTGCTGGCTGAGCCAGGCGCCCTCTCCAG	759	Qy	1780	CAGGAGGAGGTTTATCCAGCAGGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAAC	1839
Db	781	GAATGCAGCATGCAAGACCTCATCTTTCAGCTGCTGGCTGAGCCAGGCGCCCTCTCCAG	840	Db	1861	CAGGAGGAGGTTTATCCAGCAGGGCCCTGAGCCACTTCCAGGTGATCGTGGTCAGCAAC	1920
Qy	760	GAGCTCATCCGAGTCCCGAGCGCTCTTTTCATATCGACGGCTTCGATGAGCTCAAG	819	Qy	1840	ATTGCCCTCCAAGATGAGCAGCATGGTCTCTCTGTTCTGTCTGAAGCGCTGCAGGAGCGCC	1899
Db	841	GAGCTCATCCGAGTCCCGAGCGCTCTTTTCATATCGACGGCTTCGATGAGCTCAAG	900	Db	1921	ATTGCCCTCCAAGATGAGCAGCATGGTCTCTCTGTTCTGTCTGAAGCGCTGCAGGAGCGCC	1980
Qy	820	CCTTCTTTCACAGTCTTCAGGACCCCTGGTGGCTCTGCTGGGAGGAGAAACGGCCCAACG	879	Qy	1900	CAGGTGCTGCACTTTGATGCGCCACTA CAGCGCGGACCGGGGAGAACCGCGCAGGTGC	1959
Db	901	CCTTCTTTCACAGTCTTCAGGACCCCTGGTGGCTCTGCTGGGAGGAGAAACGGCCCAACG	960	Db	1981	CAGGTGCTGCACTTTGATGCGCCACTA CAGCGCGGACCGGGGAGAACCGCGCAGGTGC	2040
Qy	880	GAGCTGCTTCTTAACAGCTTAATTCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATC	939	Qy	1960	TCCGACGAGGCGCACGCTGTTGGTGCAGCTCAGACACAGAGAGCGTCTCTGCTGGAC	2019
Db	961	GAGCTGCTTCTTAACAGCTTAATTCGGAAGAGCTGCTCCCTGAGCTATCTTTGCTCATC	1020	Db	2041	TCCGACGAGGCGCACGCTGTTGGTGCAGCT --- ACCAGAGAGGACCGTCTCTGCTGGAC	2097
Qy	940	ACCACGCGCCACGGCTTTGGAGAGCTCCACCGTCTGCTGGAGCACCCGAGGCATGTG	999	Qy	2020	GCCTACAGTGAACATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGTATAGAGCTGTCT	2079
Db	1021	ACCACGCGCCACGGCTTTGGAGAGCTCCACCGTCTGCTGGAGCACCCGAGGCATGTG	1080	Db	2098	GCCTACAGTGAACATCTGGCAGCGGCCCTGTGCACCAATCCAAACCTGTATAGAGCTGTCT	2157
Qy	1000	GAGATCCTGGGCTTCTCTGAGGCGAGAAAGGAAGAAATCTTCTCAAGTATTTCCACAAT	1059	Qy	2080	CTGTACCGAAATGCCCTGGGACGCCGGGGGTGAAGCTGCTCTCAAGGACTCAGACAC	2139
Db	1081	GAGATCCTGGGCTTCTCTGAGGCGAGAAAGGAAGAAATCTTCTCAAGTATTTCCACAAT	1140	Db	2158	CTGTACCGAAATGCCCTGGGACGCCGGGGGTGAAGCTGCTCTCAAGGACTCAGACAC	2217
Qy	1060	GCAGACAGGGGGCCAAAGTCTTCAATTAOTGAGGGGCAACGAGCGCTCTCTTCCACCATG	1119	Qy	2140	CCCAACTGCAAACTTTCAGAACCTTGAGGCTGAAGGTTGCCGCATCTCCAGCTCAGCCTGC	2199
Db	1141	GCAGACAGGGGGCCAAAGTCTTCAATTAOTGAGGGGCAACGAGCGCTCTCTTCCACCATG	1200	Db	2218	CCCAACTGCAAACTTTCAGAACCTTGAGGCTGAAGAGTGGCCGCATCTCCAGCTCAGCCTGC	2277
Qy	1120	TGCTTCTGCTCCCTGCTGCTGGTGGTGTGTAACCTGCTCCAGGAGCAGCTGGAGGT	1179	Qy	2200	GAGGACCTCTCTGAGCTCTCATAGCCAAATAAGAAATTTGAAGAAGTGGATCTCAGTGGC	2259
Db	1201	TGCTTCTGCTCCCTGCTGCTGGTGGTGTGTAACCTGCTCCAGGAGCAGCTGGAGGT	1260	Db	2278	GAGGACCTCTCTGAGCTCTCATAGCCAAATAAGAAATTTGAAGAAGTGGATCTCAGTGGC	2337
Qy	1180	GGGGGGCTGTTGAGACAGACGTCCAGGACCAACCTGCTGAGTGTATAGCTCTTACCTGCTG	1239	Qy	2260	AACGGCTTGGAATCCAGGATGATGCTCTTTGCGAGGGCTGCGGCATCTCCAGGTGC	2319
Db	1261	GGGGGGCTGTTGAGACAGACGTCCAGGACCAACCTGCTGAGTGTATAGCTCTTACCTGCTG	1320	Db	2338	AACGGCTTGGAATCCAGGATGATGCTCTTTGCGAGGGCTGCGGCATCTCCCAATGC	2397
Qy	1240	AGTCTGATGCAACCGAGCGGGGGCCCCGGCTCTCAGCCCCCACCACACAGAGAGG	1299	Qy	2320	AGGCTGAGATGATTCAGTTGAGGAAGTGTTCAGCTGAGTCCGGGGCTTGTTCAGGAGTG	2379
Db	1321	AGTCTGATGCAACCGAGCGGGGGCCCCGGCTCTCAGCCCCCACCACACAGAGAGG	1380	Db	2398	AGGCTGAGATGATTCAGTTGAGGAAGTGTTCAGCTGAGTCCGGGGCTTGTTCAGGAGTG	2457
Qy	1300	TTGTGCTCTTGGGGCAGATGGGCTCTGGAATCAGAAATCTTATTTGAGGACAGGAC	1359	Qy	2380	GCTTCTGCTGCTGGCACCAACCCACATCTGTTGAGTTGGAACCTGACAGGAAATGCACCTG	2439
Db	1381	TTGTGCTCTTGGGGCAGATGGGCTCTGGAATCAGAAATCTTATTTGAGGACAGGAC	1440	Db	2458	GCTTCTGCTGCTGGCACCAACCCACATCTGTTGAGTTGGAACCTGACAGGAAATGCACCTG	2517
Qy	1360	CTCGGAAGCACGGCTAGACGGGGAGACGCTCTGCTTCTTCTCAACATGAACATCTTC	1419	Qy	2440	GAGGATTTGGGCTGAGGTTACTATGCGAGGACTGAGGCAACCCAGTCTGCAGACTACGG	2499
Db	1441	CTCGGAAGCACGGCTAGACGGGGAGACGCTCTGCTTCTTCTCAACATGAACATCTTC	1500	Db	2518	GAGGATTTGGGCTGAGGTTACTATGCGAGGACTGAGGCAACCCAGTCTGCAGACTACGG	2577
Qy	1420	CAGAAGGACATCAACTGAGAGGTAATACAGCTTATCCATGAGTTTCAGGAATTC	1479	Qy	2500	ACTTTGCTGCTGAAGATCTGCGGCTCAGCTGCTGCTGCTGCTGAGAGCTGGCCCTCAACT	2559
Db	1501	CAGAAGGACATCAACTGAGAGGTAATACAGCTTATCCACTTGAAGTTTCAGGAATTC	1560	Db	2578	ACTTTGCTGCTGAAGATCTGCGGCTCAGCTGCTGCTGCTGCTGAGAGCTGGCCCTCAACT	2637
Qy	1480	TTTGCAGCTATGACTATATCTTCGACGAGGGGAGGGCGGGGAGGCGCCAGACAGGAC	1539	Qy	2560	CTCAGCTGAACACAGACCTGAGAGCTGGAACCTGAGCTGGAATGAGCTGGGGGACCTC	2619
Db	1561	TTTGCAGCTATGACTATATCTTCGACGAGGGGAGGGCGGGGAGGCGCCAGACAGGAC	1620	Db	2638	CTCAGCTGAACACAGACCTGAGAGCTGGAACCTGAGCTGGAATGAGCTGGGGGACCTC	2697
Qy	1540	GTGACCAAGGCTGTTGACCGAGTACGGCTTTCTGAAAGGAGCTTCTTGGCACTCACGAGC	1599	Qy	2620	GGGTGCTGCTGCTGAGGGGCTCAGGCATCCCAAGCTGCAAGCTCCAGACCTCGGG	2679
Db	1621	GTGACCAAGGCTGTTGACCGAGTACGGCTTTCTGAAAGGAGCTTCTTGGCACTCACGAGC	1680	Db	2698	GGGTGCTGCTGCTGAGGGGCTCAGGCATCCCAAGCTGCAAGCTCCAGACCTCGGG	2757
Qy	1600	CGCTTCTGTTTGAACCTCTGAAACGAGGAGACGAGGACCACTGGAGAGAGTCTCTGC	1659	Qy	2680	TTGGGCACTCTGCGGCTGGGCTCTGCGGCTCTGAGGGTCTTTCTGTGTGTGCTCAGGCC	2739
Db	1681	CGCTTCTGTTTGAACCTCTGAAACGAGGAGACGAGGACCACTGGAGAGAGTCTCTGC	1740	Db	2758	TTGGGCACTCTGCGGCTGGGCTCTGCGGCTCTGAGGGTCTTTCTGTGTGTGCTCAGGCC	2817
Qy	1660	TGGAAGGTCTCGCGCACATCAAGATGACCTGTTGAGTGGATCCAAAGCAAGAGCTCAG	1719	Qy	2740	AACCAACAACCTCCGGGAGCTGGAATTCAGTTTCAACGACTGGGAGACTGGGGCTGTGG	2799
Db	1741	TGGAAGGTCTCGCGCACATCAAGATGACCTGTTGAGTGGATCCAAAGCAAGAGCTCAG	1800	Db	2818	AACCAACAACCTCCGGGAGCTGGAATTCAGTTTCAACGACTGGGAGACTGGGGCTGTGG	2877
				Qy	2800	TTGCTGCTGAGGGGCTGCAACATCCCGCTGCGAGACTCCAGAACTGTGTGCTGGATAGC	2859

Db	2878	TTGCTGGCTGAGGGGCTGCAACATCCCGCTGCAGACTCCAGAAATGTGGCTGGATAGC	2937	Qy	289	-----	288
Qy	2860	TGTGGCTCAAGCGCAAGGCTTGTGAGATCTTTACTTCACTGGGATCAACAGACC	2919	Db	418	GGTGGCCCGTCTCACTTTGGGAACCACTCAATGCTTCTGGAGTCTCTCTTTGCACT	477
Db	2938	TGTGGCTCAAGCGCAAGGCTTGTGAGATCTTTACTTCACTGGGATCAACAGACC	2997	Qy	289	-----GATCCCGAGGAAACCTACAGGGAATATGTTCGGCAGGAAATTCGGGCTCATG	339
Qy	2920	TTGACCCACCTTTACCTGACCAACAACCGCCCTAGGGGACACAGGTGTCCGACTGCTTTGC	2979	Db	478	CCRAAGAAAGATCCCGAGGAAACCTACAGGGAATATGTTCGGCAGGAAATTCGGGCTCATG	537
Db	2998	TTGACCCACCTTTACCTGACCAACAACCGCCCTAGGGGACACAGGTGTCCGACTGCTTTGC	3057	Qy	340	GAAGACCGCAATCGCGCCCTAGGGGATGTCAACTCAGCCACACCGGTACACCCGGCTC	399
Qy	2980	AAGCGGCTGAGCCATCTGCTGCAAACTCCGAGTCTCTGTTATTTGGATGGACCTG	3039	Db	538	GAAGACCGCAATCGCGCCCTAGGGGATGTCAACTCAGCCACACCGGTACACCCGGCTC	597
Db	3058	AAGCGGCTGAGCCATCTGCTGCAAACTCCGAGTCTCTGTTATTTGGATGGACCTG	3117	Qy	400	CTGCTGTGTGAAGAGAGACTCAAAACCCCATGCAGGTCCAGCAGAGTCTTGTGACACAGGC	459
Qy	3040	AATAAATGACCCACAGTAGGTTGGCAGCGCTTCGAGTAAACAAACCTTATTTGGACATT	3099	Db	598	CTGCTGTGTGAAGAGAGACTCAAAACCCCATGCAGGTCCAGCAGAGTCTTGTGACACAGGC	657
Db	3118	AATAAATGACCCACAGTAGGTTGGCAGCGCTTCGAGTAAACAAACCTTATTTGGACATT	3177	Qy	460	CGGGACACGCGGAGCCGTGGGACACAGGCTAGCCCCCATCAAGATAGAGACCTCTTT	519
Qy	3100	GGCTGCTGA 3108		Db	658	CGGGACACGCGGAGCCGTGGGACACAGGCTAGCCCCCATCAAGATAGAGACCTCTTT	717
Db	3178	GGCTGCTGA 3186		Qy	520	GAGCCAGCAGGAGCGCCCGAGCCACCGCGCACCGTGTGTCATGCAAGCGCGGACAGG	579
RESULT 6							
US-10-407-866-67							
; Sequence 67, Application US/10407866							
; Publication No. US20040002593A1							
; GENERAL INFORMATION:							
; APPLICANT: Reed, John C.							
; APPLICANT: Godzik, Adam							
; TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,							
; TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use							
; FILE REFERENCE: 66654-10 (LJ 5755)							
; CURRENT APPLICATION NUMBER: US/10/407,866							
; CURRENT FILING DATE: 2003-04-04							
; PRIOR APPLICATION NUMBER: US 60/370,538							
; PRIOR FILING DATE: 2002-04-04							
; NUMBER OF SEQ ID NOS: 129							
; SOFTWARE: FastSeq for Windows Version 4.0							
; SEQ ID NO 67							
; LENGTH: 3218							
; TYPE: DNA							
; ORGANISM: Homo sapiens							
; FEATURE:							
; NAME/KEY: CDS							
; LOCATION: (118)...(3200)							
US-10-407-866-67							
Query Match 94.2%; Score 2929; DB 17; Length 3218;							
Best Local Similarity 97.4%; Pred. No. 0;							
Matches 3020; Conservative 0; Mismatches 0; Indels 81; Gaps 1;							
Qy	1	ATGCTACGAACCGCAGCAGGAGCGGCTCTGTGCGCTGTCCACCTATTTGAAGAACTC	60	Qy	1000	GAGATCCTGGGCTTCTCTGAGGCAGAAAGAAAGAAATCTTCTACAGTATTTCCACAT	1059
Db	118	ATGCTACGAACCGCAGCAGGAGCGGCTCTGTGCGCTGTCCACCTATTTGAAGAACTC	177	Db	1198	GAGATCCTGGGCTTCTCTGAGGCAGAAAGAAAGAAATCTTCTACAGTATTTCCACAT	1257
Qy	61	GAGGCTGTGAACTGAAGAAGTTCAAGTTATACCTGGGACCGCGACAGAGCTGGAGAA	120	Qy	1060	GCAGAGAGCGCGGCGCAAGTCTTCAATTAAGTGAAGGCAACAGAGCTCTCTTCCACATG	1119
Db	178	GAGGCTGTGAACTGAAGAAGTTCAAGTTATACCTGGGACCGCGACAGAGCTGGAGAA	237	Db	1258	GCAGAGAGCGCGGCGCAAGTCTTCAATTAAGTGAAGGCAACAGAGCTCTCTTCCACATG	1317
Qy	121	GGCAAGATCCCTGGGGAAGCATGGAGAAGCGGCTCCCTGGAAATGGCCAGCTGCTC	180	Qy	1120	TGCTTGTGCTCCCTGGTGTGCTGGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1179
Db	238	GGCAAGATCCCTGGGGAAGCATGGAGAAGCGGCTCCCTGGAAATGGCCAGCTGCTC	297	Db	1318	TGCTTGTGCTCCCTGGTGTGCTGGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1377
Qy	181	ATCACCCACTTCGGGCGAGAGAGGCTGTGAGTTGTGCTCTAGCACCCTTTGAGCGGATA	240	Qy	1180	GGGGGGCTGTGTGACAGACGTCCAGGACCAACACTGCACTGTACATGTCTTACCTGCTG	1239
Db	298	ATCACCCACTTCGGGCGAGAGAGGCTGTGAGTTGTGCTCTAGCACCCTTTGAGCGGATA	357	Db	1378	GGGGGGCTGTGTGACAGACGTCCAGGACCAACACTGCACTGTACATGTCTTACCTGCTG	1437
Qy	241	AACAGGAAGCACTGTGGGAGAGGACAGAGAGAGCACTGGTGAGG-----	288	Qy	1240	AGTCTGTATGAAACCCAGAGCGGGGCGGCGGCTCCAGCCGCCACCAACACAGAGAGG	1299
Db	358	AACAGGAAGCACTGTGGGAGAGGACAGAGAGAGCACTGGTGAGG-----	417	Db	1438	AGTCTGTATGAAACCCAGAGCGGGGCGGCGGCTCCAGCCGCCACCAACACAGAGAGG	1497
				Qy	1300	TTGTGCTCTTTGGCGGAGATGGGCTCTGGAAATCAGAAATCTTATTTAGGAGCAGGAC	1359

Db 1498 |||||TTGTGCTCTTGGCGCAGATGGGCTCTGGAATCAGAAATCTTAATTTGAGGACGAGC 1557
Qy 1360 CTCGGAAGACGGGCTAGACGGGAAGACGCTCTGCTCTTCCCTCAACATGAATCTTC 1419
Db 1558 CTCGGAAGACGGGCTAGACGGGAAGACGCTCTGCTCTTCCCTCAACATGAATCTTC 1617
Qy 1420 CAGAAGGACATCAACTGTGAGAGGTACTACAGCTTCACTCACTTGAAGTTCCAGGAATTC 1479
Db 1618 CAGAAGGACATCAACTGTGAGAGGTACTACAGCTTCACTCACTTGAAGTTCCAGGAATTC 1677
Qy 1480 TTTGACAGTATGTAATCTCTGACGAGGGGAGGCGGGGAGGCGCCAGACGAGAC 1539
Db 1678 TTTGACAGTATGTAATCTCTGACGAGGGGAGGCGGGGAGGCGCCAGACGAGAC 1737
Qy 1540 GTGACACGCTGTTGACCGAGTACGCGTCTTCTGAAGGAGCTTCTTGGCACTCACACG 1599
Db 1738 GTGACACGCTGTTGACCGAGTACGCGTCTTCTGAAGGAGCTTCTTGGCACTCACACG 1797
Qy 1600 CGTTCCTGTTTGGACTCTCTGAACGAGGAGACCGAGGACCCACCTGGAGAGAGTCTCTGC 1659
Db 1798 CGTTCCTGTTTGGACTCTCTGAACGAGGAGACCGAGGACCCACCTGGAGAGAGTCTCTGC 1857
Qy 1660 TGAAGGCTCTCGCGCACATCAAGATGACCTGTTCAGTGGATCCAAAGCAAAAGCTCAG 1719
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Qy 1720 AGCGAGGCTCTCACCTCGACGAGGCTCTTGGAGTCTTTCAGTGGTCTGACGAGATC 1779
Db 1918 AGCGAGGCTCTCACCTCGACGAGGCTCTTGGAGTCTTTCAGTGGTCTGACGAGATC 1977
Qy 1780 CAGGAGGAGGATTTATCCAGCAGGCGCTGAGCCACTTCCAGGTGATCGTGGTCAAGAAC 1839
Db 1978 CAGGAGGAGGATTTATCCAGCAGGCGCTGAGCCACTTCCAGGTGATCGTGGTCAAGAAC 2037
Qy 1840 ATTGCTTCAAGATGAGACATAGTCTTCCTGCTTCTGTCTGAAGCGCTGACGAGCGCC 1899
Db 2038 ATTGCTTCAAGATGAGACATAGTCTTCCTGCTTCTGTCTGAAGCGCTGACGAGCGCC 2097
Qy 1900 CAGGTGCTGACTTGTATGGCGCCACCTACAGCGCGGAGGAGACCGCGCGAGGTGC 1959
Db 2098 CAGGTGCTGACTTGTATGGCGCCACCTACAGCGCGGAGGAGACCGCGCGAGGTGC 2157
Qy 1960 TCCGAGGAGGCGCACACGCTGTTGGTGCAGCTCAGACGAGAGGAGCGCTTCTGCTGGAC 2019
Db 2158 TCCGAGGAGGCGCACACGCTGTTGGTGCAGCTCAGACGAGAGGAGCGCTTCTGCTGGAC 2217
Qy 2020 GCCTACAGTGAACATCTGGAGCGGCGCTGTGACCAATCCAAACCTGATGAGCTGTCT 2079
Db 2218 GCCTACAGTGAACATCTGGAGCGGCGCTGTGACCAATCCAAACCTGATGAGCTGTCT 2277
Qy 2080 CTGTACCGAAATGCCCTGGCAGCGCGGGGTGAAGCTGCTCTGTCAGGACTCAGACAC 2139
Db 2278 CTGTACCGAAATGCCCTGGCAGCGCGGGGTGAAGCTGCTCTGTCAGGACTCAGACAC 2337
Qy 2140 CCCAACTGCAAACTTCAAGCTCAGGCTGAAGAGGTGCGCATCTCCAGCTCAGCGCTGC 2199
Db 2338 CCCAACTGCAAACTTCAAGCTCAGGCTGAAGAGGTGCGCATCTCCAGCTCAGCGCTGC 2397
Qy 2200 GAGGACCTCTCTGACGCTCTCATAGCCAAATGAAGATTTGAACAAGATGGATCTCAGTGGC 2259
Db 2398 GAGGACCTCTCTGACGCTCTCATAGCCAAATGAAGATTTGAACAAGATGGATCTCAGTGGC 2457
Qy 2260 AACCGGCTGTGATTTCCAGGACATGATGCTGTTTTCGAGGGGCTGCGGCATCCCCAGTGC 2319
Db 2458 AACCGGCTGTGATTTCCAGGACATGATGCTGTTTTCGAGGGGCTGCGGCATCCCCAGTGC 2517
Qy 2320 AGGCTGCAGATGATTTCACTTGAGGAAGTGTGAGCTGAGTCCGGGGCTTTGTGAGGAGATG 2379
Db 2518 AGGCTGCAGATGATTTCACTTGAGGAAGTGTGAGCTGAGTCCGGGGCTTTGTGAGGAGATG 2577
Qy 2380 GCTTCTGTGCTCGGCACCAACCTCAGATCTGTTGAGTTGACCTGACAGGAAATGCACTG 2439

Db 2578 GCTTCTGTGCTCGGCACCAACCCACATCTGTTGAGTTGGACCTGACAGGAAATGCACTG 2637
Qy 2440 GAGGATTTGGGCTCTGAGGTTACTATGCGAGGACTGAGGACACCCAGTCTGACAGACTACGG 2499
Db 2638 GAGGATTTGGGCTCTGAGGTTACTATGCGAGGACTGAGGACACCCAGTCTGACAGACTACGG 2697
Qy 2500 ACTTTGTGGCTGAAGATCTGCGGCTCACTGCTGCTCACTGCTGTGAGAGCTGGCTCAACT 2559
Db 2698 ACTTTGTGGCTGAAGATCTGCGGCTCACTGCTGCTCACTGCTGTGAGAGCTGGCTCAACT 2757
Qy 2560 CTGAGTCTGAACAGAGCCTGAGAGAGCTGGACCTGAGCCTGGAATGAGCTGGGGACCTC 2619
Db 2758 CTGAGTCTGAACAGAGCCTGAGAGAGCTGGACCTGAGCCTGGAATGAGCTGGGGACCTC 2817
Qy 2620 GGGGTGCTGCTGCTGTGTGAGGGGCTCAGGACATCCACGTCGAAGCTCCAGACCTGCGG 2679
Db 2818 GGGGTGCTGCTGCTGTGTGAGGGGCTCAGGACATCCACGTCGAAGCTCCAGACCTGCGG 2877
Qy 2680 TTGGGCAATCTGCGGCTGCGGCTCTGCGGCTGTGAGGGTCTTTCTGTGTGCTCCAGGCC 2739
Db 2878 TTGGGCAATCTGCGGCTGCGGCTCTGCGGCTGTGAGGGTCTTTCTGTGTGCTCCAGGCC 2937
Qy 2740 AACACAACTCCGGGAGCTGGACTTGAAGTTTCAACGACCTGGGAGACTGGGGCTGTGG 2799
Db 2938 AACACAACTCCGGGAGCTGGACTTGAAGTTTCAACGACCTGGGAGACTGGGGCTGTGG 2997
Qy 2800 TTGCTGCTGAGGGGCTGCAACATCCCGCTGACAGATCCAGAAATCTGTGCTGGATAGC 2859
Db 2998 TTGCTGCTGAGGGGCTGCAACATCCCGCTGACAGATCCAGAAATCTGTGCTGGATAGC 3057
Qy 2860 TTGCTGCTGAGGGGCTGCAACATCCCGCTGACAGATCCAGAAATCTGTGCTGGATAGC 2919
Db 3058 TTGCTGCTGAGGGGCTGCAACATCCCGCTGACAGATCCAGAAATCTGTGCTGGATAGC 3117
Qy 2920 TTGCTGCTGAGGGGCTGCAACATCCCGCTGACAGATCCAGAAATCTGTGCTGGATAGC 2979
Db 3118 TTGCTGCTGAGGGGCTGCAACATCCCGCTGACAGATCCAGAAATCTGTGCTGGATAGC 3177
Qy 2980 AAGCGGCTGAGCCATCTGCTGCAAACTCCGAGTCTCTG 3020
Db 3178 AAGCGGCTGAGCCATCTGCTGCAAACTCCGAGTCTCTG 3218

RESULT 7

US-10-108-260A-718
; Sequence 718, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 718
; LENGTH: 3466
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-718

Query Match 85.1%; Score 2644.2; DB 17; Length 3466;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 2931; Conservative 0; Mismatches 3; Indels 255; Gaps 3;
Qy 1 ATGCTACGAACCGCAGGAGGAGCGGCTCTGTGCTGTCCACTTACTTGAAGAACTC 60
Db 145 ATGCTACGAACCGCAGGAGGAGCGGCTCTGTGCTGTCCACTTACTTGAAGAACTC 204
Qy 61 GAGGCTCTGGAAGTGAAGAGTTCAAGTTATACCTGGGGCCGCGACAGAGCTGGAGAA 120
Db 205 GAGGCTCTGGAAGTGAAGAGTTCAAGTTATACCTGGGGCCGCGACAGAGCTGGAGAA 264

QY 121 GGCAAGATCCCTGGGGAAGCATGGAGAAAGCCGGTCCCTCGGAATGCCCCAGCTGCTC 180
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 QY 181 ATACCCCACTTCGGGCCAGAGAGGCTGGAGGTTGGCTCTCAGACACTTTTCAGCGGATA 240
 DB 325 ATACCCCACTTCGGGCCAGAGAGGCTGGAGGTTGGCTCTCAGACACTTTTCAGCGGATA 384
 QY 241 AACAGGAAGACCTGTGGGAGAGAGGACAGAGAGAGACCTGTGTGAGG-----288
 DB 385 AACAGGAAGACCTGTGGGAGAGAGGACAGAGAGAGACCTGTGTGAGGATACCCCACT 444
 QY 289 -----288
 DB 445 GGTGGCCGCTCTCACTTGGGAACCACTCAACATGCTTCTGGAAGTCTCTCTGTGCACT 504
 QY 289 -----GATCCCAAGGAACCTACAGGACATATGTCCGACAGGAATTTCCGGCTCATG 339
 DB 505 CCAAGAAAGATCCCAAGGAACCTACAGGACATATGTCCGACAGGAATTTCCGGCTCATG 564
 QY 340 GAAGACCGCAATGCGCGCTTAGGGAAATGTGTCAACCTCAGCCACCGGTACACCCGGCTC 399
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 QY 400 CTGCTGTGAAGAGGACTCAAAACCCCATGCAAGTCCAGCAGCAGCTTCTGGACACAGGC 459
 DB 625 CTGCTGTGAAGAGGACTCAAAACCCCATGCAAGTCCAGCAGCAGCTTCTGGACACAGGC 684
 QY 460 CGGGACACGAGACCGTGGGACACAGCGCTAGCCCCATCAAGATAGAGACCTCTTT 519
 DB 685 CGGGACACGAGGACCGTGGGACACAGCGCTAGCCCCATCAAGATAGAGACCTCTTT 744
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 QY 700 GAATGAGATGCAAGACTCATCTTCACTGCTGGCTGAGCCGAGCGCCCTCTCCAG 759
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 DB 1405 GGGGGGCTGTGTGAGACAGAGCTCCAGGACCAACCACTGCACTGTACATGCTCTACTCTGCTG 1464
 QY 1240 AGTCTGATGCAACCAACCGGGGCGCCCGCTCCAGCCCCCACCACCAACCAAGAGAGGG 1299
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 QY 1300 TTGTGCTCTTGGCGGAGATGGGCTCTGGAATCAGAAAAATCTTATTTGAGGAGCAGGAC 1359
 DB 1525 TTGTGCTCTTGGCGGAGATGGGCTCTGGAATCAGAAAAATCTTATTTGAGGAGCAGGAC 1584
 QY 1360 CTCGGAGACACGGCTTAGAGGGGGAAGAGTCTCTGCTTCTCTCAACATGAAATCTTCT 1419
 DB 1585 CTCGGAGACACGGCTTAGAGGGGGAAGAGTCTCTGCTTCTCTCAACATGAAATCTTCT 1644
 QY 1420 CAGAAGGACATCAACTGTGAGAGGTACTACAGCTTCTATCACTTGAAGTTTCCAGGAATTC 1479
 DB 1645 CAGAAGGACATCAACTGTGAGAGGTACTACAGCTTCTATCACTTGAAGTTTCCAGGAATTC 1704
 QY 1480 TTTCAGCTATGTACTATATCTTGAACGAGGAGGCGGGGAGGCGGAGGAGGAGGAGGAGG 1539
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 QY 1600 CGCTTCTCTTGGGACTCTCTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1659
 DB 1825 CGCTTCTCTTGGGACTCTCTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1884
 QY 1660 TGAAGGCTCTCGCGCACATCAAGATGACCTGTTGCAAGTGGATCCAAAGCAAAAGCTCAG 1719
 DB 1885 TGAAGGCTCTCGCGCACATCAAGATGACCTGTTGCAAGTGGATCCAAAGCAAAAGCTCAG 1944
 QY 1720 AGCGAGGCTCCACCTCTGAGCAGGAGGCTCTTGGAGTCTTTCAGCTGTGTGACAGATC 1779
 DB 1945 AGCGAGGCTCCACCTCTGAGCAGGAGGCTCTTGGAGTCTTTCAGCTGTGTGACAGATC 2004
 QY 1780 CAGGAGGAGGAGTTCATCCAGCAGGCGCTGAGCAGCTTCCAGGTCATGTCGTGACAGAAC 1839
 DB 2005 CAGGAGGAGGAGTTCATCCAGCAGGCGCTTGAAGCTTCCAGGTCATGTCGTGACAGAAC 2064
 QY 1840 ATTGCTCCAGATGAGGACATGTCCTCTGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1899
 DB 2065 ATTGCTCCAGATGAGGACATGTCCTCTGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2124
 QY 1900 CAGGTCGTGACATTTGATGGCGCCACCTACAGCGGAGCGGGGAGAGACCGCGGAGGTCG 1959
 DB 2125 CAGGTCGTGACATTTGATGGCGCCACCTACAGCGGAGCGGGGAGAGACCGCGGAGGTCG 2184
 QY 1960 TCCGAGGAGCGGACACGCTGTTGGTGACCTCAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGG 2019
 DB 2185 TCCGAGGAGCGGACACGCTGTTGGTGACCT---ACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2241
 QY 2020 GCCTACAGTGAACATCTGGCAGCGGCGCTGTGACCAATCCAAACCTGTATGAGTGTGCT 2079
 DB 2242 GCCTACAGTGAACATCTGGCAGCGGCGCTGTGACCAATCCAAACCTGTATGAGTGTGCT 2301
 QY 2080 CTGTACCGAAATGCCCTGGGAGCGCGGGGGTGAAGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2139
 DB 2302 CTGTACCGAAATGCCCTGGGAGCGCGGGGGTGAAGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2361
 QY 2140 CCCAACTGCAAACTTCAGAACCTGAGGCTGAAAGGTCGCGCATCTCCAGCTCAGGCTGCT 2199
 DB 2362 CCCAACTGCAAACTTCAGAACCTGAGGCTGAAAGGTCGCGCATCTCCAGCTCAGGCTGCT 2421
 QY 2200 GAGGACCTCTCTGAGCTCTCATAGGCAATGAAGATTTGACAGGATGATCTCAGTGGC 2259

181 CCACCAACACAGAGAGGGTTGTCTCTCTGGCGCAGATGGGCTCTGGAATCAGAAAAATC 240 Db
1342 CTATTTGAGAGCAGAGACCTCCGGAAGCAGCGGCTAGACGGGAAGACCTCTCTGCTTTC 1401 Qy
241 CTATTTGAGAGCAGAGACCTCCGGAAGCAGCGGCTAGACGGGAAGACCTCTCTGCTTTC 300 Db
1402 CTCAACATGAACATCTTCCAGAAAGGACATCAACTGTGAGAGTATACAGCTTCAATCCAC 1461 Qy
301 CTCAACATGAACATCTTCCAGAAAGGACATCAACTGTGAGAGTATACAGCTTCAATCCAC 360 Db
1462 TTGAGTTTCCAGGAATCTTTTGAGCTATGTATATATCTGACGAGGGAGGGCGGG 1521 Qy
361 TTGAGTTTCCAGGAATCTTTTGAGCTATGTATATATCTGACGAGGGAGGGCGGG 420 Db
1522 GCAGGCCACAGACAGGAGCTGACAGGCTGTGTACCGAGTACGCGTTTCTGAAAGGAGC 1581 Qy
421 GCAGGCCACAGACAGGAGCTGACAGGCTGTGTACCGAGTACGCGTTTCTGAAAGGAGC 480 Db
1582 TTCCTGGCACTCACAGCGGCTTCTGTTGGACTCTGAAACAGAGGACAGGAGCCAC 1641 Qy
481 TTCCTGGCACTCACAGCGGCTTCTGTTGGACTCTGAAACAGAGGACAGGAGCCAC 540 Db
1642 CTGAGAGAGTCTCTGCTGAAGTCTCGCGCACATCAAGATGAGACCTGTTGCAAGTGG 1701 Qy
541 CTGAGAGAGTCTCTGCTGAAGTCTCGCGCACATCAAGATGAGACCTGTTGCAAGTGG 600 Db
1702 ATCCAAAGCAAGCTCAGAGCGAGGCTCCACCTGACAGAGGCTCCTTGGAGTTCTTC 1761 Qy
601 ATCCAAAGCAAGCTCAGAGCGAGGCTCCACCTGACAGAGGCTCCTTGGAGTTCTTC 660 Db
1762 AGCTCTTGTACGAGATCCAGAGGAGGAGTTTATCCAGAGGCGCTGAGCCATCTCCAG 1821 Qy
661 AGCTCTTGTACGAGATCCAGAGGAGGAGTTTATCCAGAGGCGCTGAGCCATCTCCAG 720 Db
1822 GTGATCGTGTGACCAACATTCCTCCAAAGATGAGACATGCTCTCTCTGTTCTGTCG 1881 Qy
721 GTGATCGTGTGACCAACATTCCTCCAAAGATGAGACATGCTCTCTCTGTTCTGTCG 780 Db
1882 AAGCGCTGAGAGCGGCGGCTGTGCACTTGTATGGCCACCTACAGGCGGAGCGG 1941 Qy
781 AAGCGCTGAGAGCGGCGGCTGTGCACTTGTATGGCCACCTACAGGCGGAGCGG 840 Db
1942 GAAGACCGCGGAGGCTCCGAGAGCGACAGCTGTTGTGTCAGCTCAGACCAAGAG 2001 Qy
841 GAAGACCGCGGAGGCTCCGAGAGCGACAGCTGTTGTGTCAGCTCAGACCAAGAG 900 Db
2002 AGGACCGTTCTGCTGAGCGCTTACAGTGAACATCTGGCAGGCGGCTGTGACCAATCCA 2061 Qy
901 AGGACCGTTCTGCTGAGCGCTTACAGTGAACATCTGGCAGGCGGCTGTGACCAATCCA 960 Db
2062 AACCTGATAGCTGTCTGTACCGAATGCCCTGGCAGCGGGGCTGAAGCTGTC 2121 Qy
961 AACCTGATAGCTGTCTGTACCGAATGCCCTGGCAGCGGGGCTGAAGCTGTC 1020 Db
2122 TGTCAAGGACTCAGACACCCCACTGCAAACTTCAGAACCT---GAGGCTGAAGAGTGC 2178 Qy
1021 TGTCAAGGACTCAGACACCCCACTGCAAACTTCAGAACCTGAGGAGGCTGAAGAGTGC 1080 Db
2179 CGCATCTCCAGCTCAGCGCTGAGGAGCTCTCTGAGCTCTATGACCAATGAAGTTTG 2238 Qy
1081 CGCATCTCCAGCTCAGCGCTGAGGAGCTCTCTGAGCTCTATGACCAATGAAGTTTG 1140 Db
2239 ACAAGGATGATCTCAGTGCACGCGCTTGGATCCAGGAGATGATGCTGTTTCGAG 2298 Qy
1141 ACAAGGATGATCTCAGTGCACGCGCTTGGATCCAGGAGATGATGCTGTTTCGAG 1200 Db
2299 GGCCTGGGATCCCGAGTGCAGCTGCAGATGATTCAGTTGAGGAGTGTGAGCTGGAG 2358 Qy
1201 GGCCTGGGATCCCGAGTGCAGCTGCAGATGATTCAGTTGAGGAGTGTGAGCTGGAG 1260 Db
2359 TCCGGGCTTGTGAGGAGTGGCTCTGCTGCGGACCAACCAATCTGTTGAGTTG 2418 Qy
1261 TCCGGGCTTGTGAGGAGTGGCTCTGCTGCGGACCAACCAATCTGTTGAGTTG 1320 Db

2419 GACCTGACAGGAATGCACTGAGGATTTGGGCTGAGGTTTACTATGCCAGGAGCTGAGG 2478 Qy
1321 GACCTGACAGGAATGCACTGAGGATTTGGGCTGAGGTTTACTATGCCAGGAGCTGAGG 1380 Db
2479 CACCCAGTCTGACAGCTACGAGCTTTTGT-----GGCTGAAGATCTGCCCGCTCAGCTGCT 2532 Qy
1381 CACCCAGTCTGACAGCTACGAGCTTTTGTGCTGCGAGGCTGAAGATCTGCCCGCTCAGCTGCT 1440 Db
2533 GCTGCTGTGACAGCTGCGCTCAACTCTCAGTGTGAACAGAGCCTGAGAGAGCTGGAC 2592 Qy
1441 GCTGCTGTGACAGCTGCGCTCAACTCTCAGTGTGAACAGAGCCTGAGAGAGCTGGAC 1500 Db
2593 CTGAGCTGATGAGCTGGGGGAGCTCGGGGTGCTGCTGTGTGTGAGGGCCTCAGGCAT 2652 Qy
1501 CTGAGCTGATGAGCTGGGGGAGCTCGGGGTGCTGCTGTGTGTGAGGGCCTCAGGCAT 1560 Db
2653 CCCAGTGCACAGCTCCAGACCTGCG---GGTTGGGATCTGCGCGGCTGGGCTCTGCCGCC 2709 Qy
1561 CCCAGTGCACAGCTCCAGACCTGCGGGAGGTTGGGATCTGCGCGGCTGGGCTCTGCCGCC 1620 Db
2710 TGTGAGGCTCTTCTGTGTGCTCCAGGCCAACACACCTCCCGGAGCTGGAGCTTGAGT 2769 Qy
1621 TGTGAGGCTCTTCTGTGTGCTCCAGGCCAACACACCTCCCGGAGCTGGAGCTTGAGT 1680 Db
2770 TTCAACAGACCTGGGAGCTGGGGGCTGTGTTGTGTGTGAGGGGCTGCAACATCCCGCC 2829 Qy
1681 TTCAACAGACCTGGGAGCTGGGGGCTGTGTTGTGTGTGAGGGGCTGCAACATCCCGCC 1740 Db
2830 TGCAGACTCCAGAACTGTGG 2850 Qy
1741 TGCAGACTCCAGAACTGTGG 1761 Db

RESULT 9
US-10-467-397-19
; Sequence 19, Application US/10467397
; Publication No. US20040137448A1
; GENERAL INFORMATION:
; APPLICANT: THORNTON, Michael; HAFALIA, April J.A.;
; APPLICANT: LU, Dzung Aina M.; ARVIZU, Chandra S.;
; APPLICANT: SWARNAKAR, Anita; LU, Yan;
; APPLICANT: WARREN, Bridget A.; BAUGHN, Mariah R.;
; APPLICANT: TANG, Y. Tom; LEE, Ernestine A.;
; APPLICANT: YAO, Monique G.; RAMKUMAR, Jayalaxmi;
; APPLICANT: KHAN, Farrah A.; GANDHI, Ameena R.;
; APPLICANT: DING, Li; YUE, Henry;
; APPLICANT: GIETZEN, Kimberly J.; CHAWLA, Narinder K.;
; APPLICANT: THANGAVELU, Kavitha; ELLIOTT, Vicki S.
; APPLICANT: MARQUIS, Joseph P.
; TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS
; FILE REFERENCE: PI-0368 USN
; CURRENT APPLICATION NUMBER: US/10/467,397
; CURRENT FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: PCT/US02/03844
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 60/268,118
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/270,963
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,858
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/271,194
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/274,071
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/283,496
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/344,650
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19

LENGTH: 2158
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 429930CB1
US-10-467-397-19

Query Match 54.1%; Score 1681.8; DB 18; Length 2158;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

Qy 1408 ATGAACATCTCCAGAGGACATCAACTGTGAGAGTACTACAGCTTCATCCACTTGAGT 1467
Db 1 ATGAACATCTCCAGAGGACATCAACTGTGAGAGTACTACAGCTTCATCCACTTGAGT 60

Qy 1468 TTCAGAGATTTCTTTGGAGCTATCTACTATATCTGACGAGGGGAGGGGGGCGGAGGC 1527
Db 61 TTCAGAGATTTCTTTGGAGCTATCTACTATATCTGACGAGGGGAGGGGGGCGGAGGC 120

Qy 1528 CCAGACAGGAGCTGACAGGCTGTGTACCCAGTACGCGTTTCTGAAAGGAGCTTCCTG 1587
Db 121 CCAGACAGGAGCTGACAGGCTGTGTACCCAGTACGCGTTTCTGAAAGGAGCTTCCTG 180

Qy 1588 GCATCTACAGCGGCTTCCTGTTGGACTCTCTGAAACGAGGAGACAGAGGCCACTGGAG 1647
Db 181 GCATCTACAGCGGCTTCCTGTTGGACTCTCTGAAACGAGGAGACAGAGGCCACTGGAG 240

Qy 1648 AAGAGTCTCTGCGAGGCTCTCCGCGACATCAAGATGACCTGTTCAGTGGATCCAA 1707
Db 241 AAGAGTCTCTGCGAGGCTCTCCGCGACATCAAGATGACCTGTTCAGTGGATCCAA 300

Qy 1708 AGCAAAAGCTCAGAGCGAGGCTCCACCTGACGAGGCTCCTTTGGAGTCTTCAGCTGC 1767
Db 301 AGCAAAAGCTCAGAGCGAGGCTCCACCTGACGAGGCTCCTTTGGAGTCTTCAGCTGC 360

Qy 1768 TTGTACAGATCCAGAGGAGGAGTATTCAGAGGCGCTTCAGGCCACTCCAGGTGATC 1827
Db 361 TTGTACAGATCCAGAGGAGGAGTATTCAGAGGCGCTTCAGGCCACTCCAGGTGATC 420

Qy 1828 GTGCTCAGACATTTGCTCCAGATGGAGGACATGCTCTCTGTTCTGTCTGAAGGC 1887
Db 421 GTGCTCAGACATTTGCTCCAGATGGAGGACATGCTCTCTGTTCTGTCTGAAGGC 480

Qy 1888 TGCAGAGCGCCAGGCTGCTGCACTTTGATGGCGCCACCTACAGCGGCGAGCGGGAAGAC 1947
Db 481 TGCAGAGCGCCAGGCTGCTGCACTTTGATGGCGCCACCTACAGCGGCGAGCGGGAAGAC 540

Qy 1948 CGCGGAGGTGCTCCGAGGAGCGCACACGCTGTTGTGCGAGCTCAGACAGAGAGGACC 2007
Db 541 CGCGGAGGTGCTCCGAGGAGCGCACACGCTGTTGTGCGAGCTCAGACAGAGAGGACC 597

Qy 2008 GTTCTGTGGAGCGCTACAGTGAACATCTGCGAGGCGCTGTGACCCATCCAAACCTG 2067
Db 598 GTTCTGTGGAGCGCTACAGTGAACATCTGCGAGGCGCTGTGACCCATCCAAACCTG 657

Qy 2068 ATAGAGTGTCTGTATCCGAAATGCCCTGGCGAGCGGGGGTGAAGCTGCTCTGTCAA 2127
Db 658 ATAGAGTGTCTGTATCCGAAATGCCCTGGCGAGCGGGGGTGAAGCTGCTCTGTCAA 717

Qy 2128 GGACTCAGACACCCCAACTGCAAACTTCAGAACTGAGGCTGAAGAGGTGCCGATCTCC 2187
Db 718 GGACTCAGACACCCCAACTGCAAACTTCAGAACTGAGGCTGAAGAGGTGCCGATCTCC 777

Qy 2188 AGCTCAGCTGGAGGAGCTCTGCGAGCTCTCATAGCAATAGAATTTGACAAGATG 2247
Db 778 AGCTCAGCTGGAGGAGCTCTGCGAGCTCTCATAGCAATAGAATTTGACAAGATG 837

Qy 2248 GATCTCAGTGCACCGGCTTGGATTCAGGAGGATGCTGCTTTTGGAGGGCTCGGG 2307
Db 838 GATCTCAGTGCACCGGCTTGGATTCAGGAGGATGCTGCTTTTGGAGGGCTCGGG 897

Qy 2308 CATCCCCAGTGCAGGCTGCAGATGATTCAGTTGAGGAAGTGTACGTGGAGTCCGGGCT 2367

Db 898 CATCCCCAATGCGAGGCTGCAGATGATTCAGTTGAGGAAGTGTACGTGGAGTCCGGGCT 957
Qy 2368 TGTCCAGAGATGGCTTCTGTGCTCGGCACCAACCCACATCTGGTTGAGTTGAGCTGACA 2427
Db 958 TGTCCAGAGATGGCTTCTGTGCTTGGACCAACCCACATCTGGTTGAGTTGAGCTGACA 1017
Qy 2428 GGAATATGCTGAGGATTTGGGCTGAGGTTACTATGCCAGGAGCTGAGGACCCAGTCT 2487
Db 1018 GGAATATGCTGAGGATTTGGGCTGAGGTTACTATGCCAGGAGCTGAGGACCCAGTCT 1077
Qy 2488 TGCAGACTACGAGTGTGGCTGAGAGCTGCGGCTCACTGCTGCTGCTGAGGAG 2547
Db 1078 TGCAGACTACGAGTGTGGCTGAGAGCTGCGGCTCACTGCTGCTGCTGAGGAG 1137
Qy 2548 CTGCGCTCAACTCTCAGTGTGAACAGAGCTGAGAGAGCTGGAACCTGAGCTTGAATGAG 2607
Db 1138 CTGCGCTCAACTCTCAGTGTGAACAGAGCTGAGAGAGCTGGAACCTGAGCTTGAATGAG 1197
Qy 2608 CTGCGGAGCTCCTGGGCTGCTGCTGTGTGAGGAGCTCAGGAGATCCCAAGTCAAGTCT 2667
Db 1198 CTGCGGAGCTCCTGGGCTGCTGCTGTGTGAGGAGCTCAGGAGATCCCAAGTCAAGTCT 1257
Qy 2668 CAGACCTGCGGTTGGGCTGCTGCGGCTGCGGCTGCTGCGGCTGCTGAGGCTCTTCTGTG 2727
Db 1258 CAGACCTGCGGTTGGGCTGCTGCGGCTGCGGCTGCTGCGGCTGCTGAGGCTCTTCTGTG 1317
Qy 2728 GTGCTCAGGAGCTCAGGAGCTGCGGAGCTGAGCTTGAAGTTCAACGAGCTCGGAGAC 2787
Db 1318 GTGCTCAGGAGCTCAGGAGCTGCGGAGCTGAGCTTGAAGTTCAACGAGCTCGGAGAC 1377
Qy 2788 TGGGCGCTGTGTTGCTGCTGAGGAGCTGCAACATCCCGCTGAGGCTCAGAGAACTG 2847
Db 1378 TGGGCGCTGTGTTGCTGCTGAGGAGCTGCAACATCCCGCTGAGGAGCTCAGAGAACTG 1437
Qy 2848 TGGCTGATGAGTGTGCGCTCAGAGCAAGGCTTGTGAGATCTTTTACTTACCTCGGCTGGG 2907
Db 1438 TGGCTGATGAGTGTGCGCTCAGAGCAAGGCTTGTGAGATCTTTTACTTACCTCGGCTGGG 1497
Qy 2908 ATCAACAGAGCTTGTGAGGAGCTTACCTGACCAACAGGCTTGTGAGGAGCTCAGAGAACTG 2967
Db 1498 ATCAACAGAGCTTGTGAGGAGCTTACCTGACCAACAGGCTTGTGAGGAGCTCAGAGAACTG 1557
Qy 2968 CGACTGCTTTGAGGAGCTGAGGAGCTTGTGAGGAGCTTGTGAGGAGCTTGTGAGGAGCT 3027
Db 1558 CGACTGCTTTGAGGAGCTGAGGAGCTTGTGAGGAGCTTGTGAGGAGCTTGTGAGGAGCT 1617
Qy 3028 GGGATGAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3087
Db 1618 GGGATGAGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1677
Qy 3088 TATTTGAGATTTGGCTGCTGA 3108
Db 1678 TATTTGAGATTTGGCTGCTGA 1698

RESULT 10

US-10-029-386-24660/c
; Sequence 24660, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24660
; LENGTH: 1704

Wed Feb 9 10:22:12 2005

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008753.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.37
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EST HUMAN HIT: AW673661.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P33076, EVALUE 4.00e-13
OTHER INFORMATION: NT HIT: g14731965, EVALUE 1.00e-07
US-10-029-386-24660
Query Match 54.1%; Score 1680; DB 16; Length 1704;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 290 ATCCCGAGGAACCTACAGGACTATGTCGCGAGGAATTCGGCTCATGGAAGACCGCA 349
DB 1704 ATCCCGAGGAACCTACAGGACTATGTCGCGAGGAATTCGGCTCATGGAAGACCGCA 1645
QY 350 ATGCGCGCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCTCTGCTGTGA 409
DB 1644 ATGCGCGCTAGGGGAATGTGTCAACCTCAGCCACCGGTACACCCGGCTCTCTGCTGTGA 1585
QY 410 AGGAGCACTCAAAACCCATGAGTCCAGAGAGAGTCTTGGACACAGGCGCGGGACAG 469
DB 1584 AGGAGCACTCAAAACCCATGAGTCCAGAGAGAGTCTTGGACACAGGCGCGGGACAG 1525
QY 470 CGAGGACCGTGGGACACAGGCTAGCCCATCAAGATAGAGACCTCTTTGAGCCAGACG 529
DB 1524 CGAGGACCGTGGGACACAGGCTAGCCCATCAAGATAGAGACCTCTTTGAGCCAGACG 1465
QY 530 AGGAGCGCCCGAGCCACCGCGCACCGTGTGTCATGCAAGCGCGGAGGATAGGCAAGT 589
DB 1464 AGGAGCGCCCGAGCCACCGCGCACCGTGTGTCATGCAAGCGCGGAGGATAGGCAAGT 1405
QY 590 CCATGCTGGCACACAGGTGATGCTGGAGTGGCGGAGCGGAAGCTCTTCCAAGGCAGAT 649
DB 1404 CCATGCTGGCACACAGGTGATGCTGGAGTGGCGGAGCGGAAGCTCTTCCAAGGCAGAT 1345
QY 650 TTGATTATCTCTTACATCACTGACGAGAGATGAACAGAGTGCCACCGAATGCGACGA 709
DB 1344 TTGATTATCTCTTACATCACTGACGAGAGATGAACAGAGTGCCACCGAATGCGACGA 1285
QY 710 TCCAGAGACTATCTTACAGTCTGCTGCTGAGCCAGCGCCCTTCCAGAGAGTCAATCC 769
DB 1284 TCCAGAGACTATCTTACAGTCTGCTGCTGAGCCAGCGCCCTTCCAGAGAGTCAATCC 1225
QY 770 GAGTTCGCGAGCGCTCTCTTTTCATCATCGACGGCTTCGATGAGCTCAAGCTCTTTTCC 829
DB 1224 GAGTTCGCGAGCGCTCTCTTTTCATCATCGACGGCTTCGATGAGCTCAAGCTCTTTTCC 1165
QY 830 ACGATCCTCAGGAGACCTGCTGCTCTGCTGGAGGAGAAACCGGCCACCGAGTGTCTTC 889
DB 1164 ACGATCCTCAGGAGACCTGCTGCTCTGCTGGAGGAGAAACCGGCCACCGAGTGTCTTC 1105
QY 890 TTAAACAGCTTAATTGGGAAGAGTCTCTCTGAGCTATCTTTGCTCATCAACACGCGC 949
DB 1104 TTAAACAGCTTAATTGGGAAGAGTCTCTCTGAGCTATCTTTGCTCATCAACACGCGC 1045
QY 950 CCACGCTTTGGAGAGCTCCACCGCTCTGCTGGAGCACCCACCGCATGTGGAGATCTCTGG 1009
DB 1044 CCACGCTTTGGAGAGCTCCACCGCTCTGCTGGAGCACCCACCGCATGTGGAGATCTCTGG 985
QY 1010 GCTTCTCTGAGGAGAAAGAGGAATACTTCTACAGTATTTCCACATGCGAGAGCAGG 1069
DB 984 GCTTCTCTGAGGAGAAAGAGGAATACTTCTACAGTATTTCCACATGCGAGAGCAGG 925
QY 1070 CGGGCAAGCTCTCAATTAGTCAGGAGCAACGAGCTCTCTTCCACATGCTCTCTGCTCC 1129
DB 924 CGGGCAAGCTCTCAATTAGTCAGGAGCAACGAGCTCTCTTCCACATGCTCTCTGCTCC 865
QY 1130 CCCTGTGTGCTGGGTGGTGTGTACTCTGCTCCAGCAGCTGAGGAGTGGGGGCTGT 1189

DB 864 CCCTGTGTGCTGGGTGGTGTGTACTCTGCTCCAGCAGCAGCTGGAGGGTGGGGGCTGT 805
QY 1190 TGAGACAGACGTCAGGACCAACCACTGCTGAGTGTATGCTCTTACCTGCTGAGTGTATGC 1249
DB 804 TGAGACAGACGTCAGGACCAACCACTGCTGAGTGTATGCTCTTACCTGCTGAGTGTATGC 745
QY 1250 AACCACAGCGGG 1309
DB 744 AACCACAGCGGG 685
QY 1310 TGGGGGAGATGGGCTCTGGAATCAGAAATCTTATTTGGAGGACAGGACCTCCGGAAGC 1369
DB 684 TGGGGGAGATGGGCTCTGGAATCAGAAATCTTATTTGGAGGACAGGACCTCCGGAAGC 625
QY 1370 ACGGCTTAGACGGGGAAGACGCTCTGCTGCTTCTTCAACATGAACATCTTCCAGAGGACA 1429
DB 624 ACGGCTTAGACGGGGAAGACGCTCTGCTGCTTCTTCAACATGAACATCTTCCAGAGGACA 565
QY 1430 TCAACTGTGAGAGGTACTACAGCTTCACTTCTGAGTTTCCAGGAAATTTCTTGCAGCTA 1489
DB 564 TCAACTGTGAGAGGTACTACAGCTTCACTTCTGAGTTTCCAGGAAATTTCTTGCAGCTA 505
QY 1490 TGTACTATATCTTGACAGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1549
DB 504 TGTACTATATCTTGACAGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 445
QY 1550 TGTGACCGAGTACCGCTTTTCTGAAAGGAGCTTCTGCTGCACTCACAGCGCTTCTCTGT 1609
DB 444 TGTGACCGAGTACCGCTTTTCTGAAAGGAGCTTCTGCTGCACTCACAGCGCTTCTCTGT 385
QY 1610 TTGGACTCTCTGAAACGAGGAGACAGGAGCCACCTGGAGAGAGTCTTCTGCGAAGGTCT 1669
DB 384 TTGGACTCTCTGAAACGAGGAGACAGGAGCCACCTGGAGAGAGTCTTCTGCGAAGGTCT 325
QY 1670 CCGCGCACATCAAGATGAGACCTTGTTCAGTGGATCCAAAGCAAGCTCAGAGCGACGCT 1729
DB 324 CCGCGCACATCAAGATGAGACCTTGTTCAGTGGATCCAAAGCAAGCTCAGAGCGACGCT 265
QY 1730 CCACCTGACAGCGGCTCTTGGAGTCTTTCAGCTGCTTGTGACGAGATCCAGGAGGAGG 1789
DB 264 CCACCTGACAGCGGCTCTTGGAGTCTTTCAGCTGCTTGTGACGAGATCCAGGAGGAGG 205
QY 1790 AGTTTATCCAGAGGCGCTTGAGCCACTTCCAGGTGATGCTGTCAGCAACATTTGCTCCA 1849
DB 204 AGTTTATCCAGAGGCGCTTGAGCCACTTCCAGGTGATGCTGTCAGCAACATTTGCTCCA 145
QY 1850 AGATGAGACATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1908
DB 144 AGATGAGACATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 85
QY 1909 CACTTGTGTA-TGGCGCCACCTACAGCGCGGAGGAGAACCGCGGAGGTGTCTCCGAGG 1967
DB 84 CACTTGTGTA-TGGCGCCACCTACAGCGCGGAGGAGAACCGCGGAGGTGTCTCCGAGG 25
QY 1968 AGCGCACACGCTCTTGGTGCAGCT 1991
DB 24 AGCGCACACGCTCTTGGTGCAGCT 1

RESULT 11
US-10-028-374-1
; Sequence 1, Application US/10028374
; Publication No. US20030143706A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; FILE REFERENCE: D0067NP
; CURRENT APPLICATION NUMBER: US/10/028,374
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/257,773
; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 4931

; TYPE: DNA

; ORGANISM: homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1320)..(2666)

US-10-028-374-1

Query Match 52.0%; Score 1616; DB 15; Length 4931;

Best Local Similarity 81.0%; Pred. No. 0;

Matches 2160; Conservative 0; Mismatches 5; Indels 501; Gaps 4;

Qy 289 GATCCCCAGGAAACCTCAGGGACTATGTCCGCGAGAAATTCGGCTCATGGAGACCGC 348

Db 1021 GATCCCCAGGAAACCTCAGGGACTATGTCCGCGAGAAATTCGGCTCATGGAGACCGC 1080

Qy 349 AATGGCGCCTTAGGGAAATGTGTAACCTCAGCCACCGGTACACCCGGCTCCTGTGGTG 408

Db 1081 AATGGCGCCTTAGGGAAATGTGTAACCTCAGCCACCGGTACACCCGGCTCCTGTGGTG 1140

Qy 409 AAGGAGCACTCAAAACCCCATCAGTCCAGCAGCAGCTTCCTGGACACAGGCCGGGACAC 468

Db 1141 AAGGAGCACTCAAAACCCCATCAGTCCAGCAGCAGCTTCCTGGACACAGGCCGGGACAC 1200

Qy 469 GCGAGGACCGTGGGACACACAGGCTAGCCCCATCAAGATAGAGACCTCTTTGAGCCAGAC 528

Db 1201 GCGAGGACCGTGGGACACACAGGCTAGCCCCATCAAGATAGAGACCTCTTTGAGCCAGAC 1260

Qy 529 GAGGAGCGCCCGAGCCACCGCGCACCGTGTCTATGCAAGCGCGGAGGAGATAGGAAG 588

Db 1261 GAGGAGCGCCCGAGCCACCGCGCACCGTGTCTATGCAAGCGCGGAGGAGAT 1313

Qy 589 TCCATGCTGGCACACAGGTGATGCTGCACTGGCGGAGCGGAAGCTCTTCCAGGCAGA 648

Db 1314 ----- 1313

Qy 649 TTTGATTATCTTTCTACATCAACTGCAGGGAGATGAACAGAGTGCACCGAATGCAGC 708

Db 1314 -----AGGAGATGAACAGAGTGCACCGAATGCAGC 1346

Qy 709 ATGCAAGACCTCATCTTCAGCTGTGGCTGAGCCACGCGCTCTCCAGGAGCTCATC 768

Db 1347 ATGCAAGACCTCATCTTCAGCTGTGGCTGAGCCACGCGCTCTCCAGGAGCTCATC 1406

Qy 769 CGAGTCCCGAGCGCCTCTTTTCATCATCGACGGCTTCGATGAGCTCAAGCCTCTTTC 828

Db 1407 CGAGTCCCGAGCGCCTCTTTTCATCATCGACGGCTTCGATGAGCTCAAGCCTCTTTC 1466

Qy 829 CACGATCCTCAGGGACCTGGTGCTCTGCTGGGAGGAGAAACGGCCACCGAGCTGCTT 888

Db 1467 CACGATCCTCAGGGACCTGGTGCTCTGCTGGGAGGAGAAACGGCCACCGAGCTGCTT 1526

Qy 889 CTTAACAGCTTAAATTCGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACACACGG 948

Db 1527 CTTAACAGCTTAAATTCGGAAGAAGCTGCTCCCTGAGCTATCTTTGCTCATCACACACGG 1586

Qy 949 CCCAGGCTTTGGAGAGCTCCACGCTCTGCTGGAGCACCCAGCATGTGGATCCTG 1008

Db 1587 CCCAGGCTTTGGAGAGCTCCACGCTCTGCTGGAGCACCCAGCATGTGGATCCTG 1646

Qy 1009 GGCTTCTCTGAGGACGAAGAAGGAATACTTCTACAAGTATTTCCAAATGCAGAGCAG 1068

Db 1647 GGCTTCTCTGAGGACGAAGAAGGAATACTTCTACAAGTATTTCCAAATGCAGAGCAG 1706

Qy 1069 GCGGCCCAAGTCTTCAATTAAGTGGGACAAACGAGCCTCTCTTCAACATGTCTCGTC 1128

Db 1707 GCGGCCCAAGTCTTCAATTAAGTGGGACAAACGAGCCTCTCTTCAACATGTCTCGTC 1766

Qy 1129 CCCCTGGTGTCTGGTGGTGTGTACTGCTCTCAGCAGCAGCTGGAGGGTGGGGGCTG 1188

Db 1767 CCCCTGGTGTCTGGTGGTGTGTACTGCTCTCAGCAGCAGCTGGAGGGTGGGGGCTG 1826

Qy 1189 TTGAGACAGACGTCCAGGACCAACCACTGCAGTGTACATGTCTCTACCTGCTGAGTCTGATG 1248

Db 1827 TTGAGACAGACGTCCAGGACCAACCACTGCAGTGTACATGTCTCTACCTGCTGAGTCTGATG 1886

Qy 1249 CAACCCAAAGCGGGGGCCCCGCGCTCCAGCCCCACCCAAACGAGAGAGGGTTGTCTCC 1308

Db 1887 CAACCCAAAGCGGGGGCCCCGCGCTCCAGCCCCACCCAAACGAGAGAGGGTTGTCTCC 1946

Qy 1309 TTGCGGCGAGATGGGCTCTGGAATCAGAAATCTATTGAGGAGCAGGACCTCCGGAAG 1368

Db 1947 TTGCGGCGAGATGGGCTCTGGAATCAGAAATCTATTGAGGAGCAGGACCTCCGGAAG 2006

Qy 1369 CACGSCCTAGACGCGGGAAGACGTCTCTGSCCTTCTCAACATGAACATCTTCCAGAAGGAC 1428

Db 2007 CACGSCCTAGACGCGGGAAGACGTCTCTGSCCTTCTCAACATGAACATCTTCCAGAAGGAC 2066

Qy 1429 ATCAACTGTGAGAGGTACTACAGCTTCATCCACTTTGAGTTTCCAGGAATCTTTTGACGT 1488

Db 2067 ATCAACTGTGAG----- 2078

Qy 1489 ATGTAATATATCTCTGGACGAGGGGGAGGGCGGCGGAGGACCTGACACAGG 1548

Db 2079 ----- 2078

Qy 1549 CTGTTGACCGAGTACGCGTTTCTGAAAGGAGCTTCTTGGCACTTCCAGCGCGCTTCTG 1608

Db 2079 -----AGGAGCTTCTTGGCACTTCCAGCGCGCTTCTG 2111

Qy 1609 TTTGGACTCTCTGAACGAGGAGACAGAGGCCACCTGGAGAAGAGTCTCTGCTGGAAGGTC 1668

Db 2112 TTTGGACTCTCTGAACGAGGAGACAGAGGCCACCTGGAGAAGAGTCTCTGCTGGAAGGTC 2171

Qy 1669 TCGCGGCACATCAAGATGGACCTGTTGCACTGGAATCCAAAGCAAGCTCAGAGGACGCGC 1728

Db 2172 TCGCGGCACATCAAGATGGACCTGTTGCACTGGAATCCAAAGCAAGCTCAGAGGACGCGC 2231

Qy 1729 TCCACCTCTGACGAGGCTCTCTTGGAGTTCTTTCAGCTGCTTGTACGAGATCCAGAGGAG 1788

Db 2232 TCCACCTCTGACGAGGCTCTCTTGGAGTTCTTTCAGCTGCTTGTACGAGATCCAGAGGAG 2291

Qy 1789 GAGTTTATCAGACGAGGCTTACAGCACTTCCAGGTGATCGTGTGTCAGCAACATTGCTCTCC 1848

Db 2292 GAGTTTATCAGACGAGGCTTACAGCACTTCCAGGTGATCGTGTGTCAGCAACATTGCTCTCC 2351

Qy 1849 AAGATGAGACACATGCTCTCTGTTCTGTAAGCGCTGCGAGGCGCCAGCTGCTG 1908

Db 2352 AAGATGAGACACATGCTCTCTGTTCTGTAAGCGCTGCGAGGCGCCAGCTGCTG 2411

Qy 1909 CACTTGTATGGCGCACCTACAGCGCGGACGGGAGAACCGCGGAGGTGCTCCGCGAGGA 1968

Db 2412 CACTTGTATGGCGCACCTACAGCGCGGACGGGAGAACCGCGGAGGTGCTCCGCGAGGA 2471

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Db 2472 GCGCACACGCTTTGTTGTCAGCT---ACCAGAGAGGACCGTTTCTGTGAGACGCTACAGT 2528

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Qy 2089 AATGCCCTTGGCGAGCCGGGGTGAAGCTGCTGTCAAGGACTCAGACACCCCACTGTC 2148

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Qy 2149 AAACCTCAGAAACCTGA----- 2164

Db 2649 AAACCTCAGAAACCTGAGGTAAAAATTTATCATATATAATATATTTTGAATAAATAATA 2708

Qy 2165 ----- 2164

Db 2709 TTGGCCAGGTATGATGGCTCAGCCTGTAAATTCAGCACCTTTTGGGAGGCCAGATGGGGA 2768

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Db		2769	GGATCACTTGACCCAGGAGTTCAAGACCAGCCTGGGCCAACATGGTGAAACCCCATCTCTA	2828
QY		2165	-----	2164
Db		2829	CTAAAAATACCAAAATAGCAGCGATGGTGGCACAAGTCTGTAGCCAGCTACTCAGG	2888
QY		2165	-----	2179
Db		2889	AGGCCAAGCAGGAGGATTCTTCAACCCAGGAGGAGAGTTGTGGCTGAAGAGGTGCC	2948
QY		2180	GCATCTCCAGCTAGCCTGCGAGGACCTCTCTCGAGCTCTCATAGCCCAATAGAAATTTGA	2239
Db		2949	GCATCTCCAGCTAGCCTGCGAGGACCTCTCTCGAGCTCTCATAGCCCAATAGAAATTTGA	3008
QY		2240	CMAGGATGGATCTCAGTGGCAACCGCGTTGGATTCCAGGCATGATGCTGTTGCGAGG	2299
Db		3009	CAAGGATGGATCTCAGTGGCAACCGCGTTGGATTCCAGGCATGATGCTGTTGCGAGG	3068
QY		2300	GCCTGCGGCATCCCGAGTGCAGGCTGCAGATGATTCAGTTGAGGAAGTGTACGTGGAGT	2359
Db		3069	GCCTGCGGCATCCCGAGTGCAGGCTGCAGATGATTCAGTTGAGGAAGTGTACGTGGAGT	3128
QY		2360	CCGGGGCTTGTGAGGATGGCTTCTGCTCGGCACCAACCCACATCTGTTGAGTTGG	2419
Db		3129	CCGGGGCTTGTGAGGATGGCTTCTGCTGGCCACCAACCCACATCTGTTGAGTTGG	3188
QY		2420	ACCTGACAGGAATGCACTGAGGATTTGGCCCTGAGGTTACTATGCCAGGCACTGAGGC	2479
Db		3189	ACCTGACAGGAATGCACTGAGGATTTGGCCCTGAGGTTACTATGCCAGGCACTGAGGC	3248
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QY		2540	GTGAGGAGTGGCTCAACTCTCAGTGTGAACAGAGCCTGAGAGAGCTGGACCTGAGCC	2599
Db		3309	GTGAGGAGTGGCTCAACTCTCAGTGTGAACAGAGCCTGAGAGAGCTGGACCTGAGCC	3368
QY		2600	TGAATGAGCTGGGAGACCTCGGGTGTGCTGTGTGAGGGCTCAGGCATCCACGT	2659
Db		3369	TGAATGAGCTGGGAGACCTCGGGTGTGCTGTGTGAGGGCTCAGGCATCCACGT	3428
QY		2660	GCAAGCTCCAGACCTCGGGTGGGC	2685
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OTHER INFORMATION:		US-10-183-770-1		
		Query Match 52.0%; Score 1616; DB 16; Length 4931;		
		Best Local Similarity 81.0%; Pred. No. 0;		
		Matches 2160; Conservative 0; Mismatches 5; Indels 501; Gaps 4;		
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		1021 GATCCCAAGGAACTTACAGGACTATGTCCGAGGAAATTCGGCTCATGGAAGCCG 1080		
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		349 AATCGCGCTTACGAGGAAATGTCAACTCAGCCACCGGTACACCCGGCTCTCTCGTG 408		
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		QY		
		409 AAGGAGCACTCAAAACCCCATGCAGTCCAGCAGCAGCTTCTGGACACAGGCCGGGACAC 468		
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		1261 GAGGAGCGCCCGAGCCACCGCGCACCGTGTCTGCAAGCGCGGAGGAT 1313		
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		1407 CGAGTTCCCGAGCGCTCCTTTTCACTCATCGACGCTTCTGATGAGCTCAAGCTCTTTC 1466		
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		1467 CAGGATCTCAGGACCTCTGCTGCTGCTGAGGAGGAAACGCGCCACCGAGCTGCTT 1526		
		QY		
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		1527 CTTAACAGCTTAATTCGGAAGAGTGTCTCCCTGAGCTATCTTGTCTATCAACCAACGG 1586		
		QY		
		949 CCCACGGCTTTGAGAGCTCCAACGCTGCTGAGGACCCAGGATGTGGATCCCTG 1008		
		1587 CCCACGGCTTTGAGAGCTCCAACGCTGCTGAGGACCCAGGATGTGGATCCCTG 1646		
		QY		
		1009 GGCTTCTCAGGACGAAAGGAGGAAATCTTCTACAAGTATTTCACAATGAGAGCAG 1068		
		1647 GGCTTCTCAGGACGAAAGGAGGAAATCTTCTACAAGTATTTCACAATGAGAGCAG 1706		
		QY		
		1069 GCGGGCCAGTCTTCAATTAAGTACGAGGAGCAACAGGCTCTCTTCAACATGCTCTGCTC 1128		
		1707 GCGGGCCAGTCTTCAATTAAGTACGAGGAGCAACAGGCTCTCTTCAACATGCTCTGCTC 1766		
		QY		
		1129 CCCTTGCTGCTGGTGGTGTGTACTGCTCCAGCAGCAGCTGAGGAGGAGGAGGCTG 1188		
		1767 CCCTTGCTGCTGGTGGTGTGTACTGCTCCAGCAGCAGCTGAGGAGGAGGAGGCTG 1826		
		QY		
		1189 TTGAGACAGACGCTCCAGGACCACTGCTGAGTGTACATGCTCTTACCTGCTGATG 1248		
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		QY		
		1249 CAACCCAAAGCGGGGGCGCCCGGCTCCAGCCCCCAGGAGGAGGAGGAGGAGGAGG 1308		

Db 1887 CAACCAAGCCGGGGCCCCGGCCTCCAGCCCCCACCACCAACAGAGAGGGTTGTGCTCC 1946
Qy 1309 TTGGCGGAGATGGGCTCTGGAATCAGAAATCTTATTTAGGAGCAGGACCTCCGGGAG 1368
Db 1947 TTGGCGGAGATGGGCTCTGGAATCAGAAATCTTATTTAGGAGCAGGACCTCCGGGAG 2006
Qy 1369 CACGCGCTAGACGGGGAAGAGTCTCTGCTCTCTCTCAACATGAACATCTTCAGAGGAC 1428
Db 2007 CACGCGCTAGACGGGGAAGAGTCTCTGCTCTCTCTCAACATGAACATCTTCAGAGGAC 2066
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Db 2067 ATCAACTGTGAG----- 2078
Qy 1489 ATGTAATAATCTCTGGACGAGGGGAGGCGGGCAGGCCAGACAGGACGTGACCAAG 1548
Db 2079 ----- 2078
Qy 1549 CTGTTGACCGAGTACCGGTTTCTGAAAGGAGCTTCCTGGGCACTCACAGCGGCTTCCTG 1608
Db 2079 -----AGGAGCTTCCTGGCACTCACAGCGGCTTCCTG 2111
Qy 1609 TTTGGACTCTGAACGAGGAGACAGGAGCCACCTGGGAGAAGTCTCTGCTGGAAGTC 1668
Db 2112 TTTGGACTCTGAACGAGGAGACAGGAGCCACCTGGGAGAAGTCTCTGCTGGAAGTC 2171
Qy 1669 TCGCGGCACATCAAGATGGACCTGTTGAGTGGATCCAAAGCAAAGCTCAGAGGACGGC 1728
Db 2172 TCGCGGCACATCAAGATGGACCTGTTGAGTGGATCCAAAGCAAAGCTCAGAGGACGGC 2231
Qy 1729 TCCACCTTGACGAGGAGCTCTTGAGTCTTTCAGTCTGTTGACGAGATCCAGAGGAG 1788
Db 2232 TCCACCTTGACGAGGAGCTCTTGAGTCTTTCAGTCTGTTGACGAGATCCAGAGGAG 2291
Qy 1789 GAGTTTATCCAGCAGGCGCTCAGCCACTTCAGGTGATCGGTGATCAGCAATGTCCTCC 1848
Db 2292 GAGTTTATCCAGCAGGCGCTCAGCCACTTCAGGTGATCGGTGATCAGCAATGTCCTCC 2351
Qy 1849 AAGATGGACACATGTTCT 1908
Db 2352 AAGATGGACACATGTTCT 2411
Qy 1909 CACTTGTATGGCGCACCTCAGCGCGGACCGGGAGACCGCGGAGGTGTCTCCGAGGA 1968
Db 2412 CACTTGTATGGCGCACCTCAGCGCGGACCGGGAGACCGCGGAGGTGTCTCCGAGGA 2471
Qy 1969 GCGCACGCTGTTGTTGTCAGTCCAGCAGAGGAGCGGTTCTCTGAGCGCTACAGT 2028
Db 2472 GCGCACGCTGTTGTTGTCAGT---ACCAGAGGAGCGGTTCTCTGAGCGCTACAGT 2528
Qy 2029 GAACATCTGGCAGCGGCGCTCTGCAACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGA 2088
Db 2529 GAACATCTGGCAGCGGCGCTCTGCAACCAATCCAAACCTGATAGAGCTGTCTCTGTACCGA 2588
Qy 2089 AATGCCCTGGGAGCGCGGGGGTGAAGTGTCTGTCTGAAGACTCAGACACCCCACTGTC 2148
Db 2589 AATGCCCTGGGAGCGCGGGGGTGAAGTGTCTGTCTGAAGACTCAGACACCCCACTGTC 2648
Qy 2149 AAACCTTCAGAACCTGA----- 2164
Db 2649 AAACCTTCAGAACCTTCAGTAAATATATATATATATATATATATATATATATATATATAT 2708
Qy 2165 ----- 2164
Db 2709 TTGGCCAGGTATGAGGCTCAGCGCTGTAAATCCAGCACTTTGGGAGGCCAGATGGGA 2768
Qy 2165 ----- 2164
Db 2769 GGATCACTTGACCCAGGAGTTCAAGACCGAGCTGGCCAAACATGGTGAACCCCATCTCTA 2828
Qy 2165 ----- 2164
Db 2829 CTAATAATAACAAATAGCAGGAGTGGTGGCACAGCTGTGTAAGCCCACTACTCAGG 2888

Qy 2165 -----GGCTGAAGAGGTGCC 2179
Db 2889 AGGCAAGGCAGGAGGATTGCTTCAACCCAGGAGGACAGGTTGTGGCTGAAGAGGTGCC 2948
Qy 2180 GCATCTCCAGTCCAGCTCGGAGGACCTCTCTGAGCTCTCATAGCCCAATGAATTTGA 2239
Db 2949 GCATCTCCAGTCCAGCTCGGAGGACCTCTCTGAGCTCTCATAGCCCAATGAATTTGA 3008
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Db 3009 CAAGATGGATCTCAGTGGCAACGGCGTTGGATTCCAGGCAATGATGCTGTTTGCAGG 3068
Qy 2300 GCCTGCGGCATCCCAAGTGCAGGCTGCAGATGATTTCAGTTGAGGAAGTGTGAGTGGAGT 2359
Db 3069 GCCTGCGGCATCCCAAGTGCAGGCTGCAGATGATTTCAGTTGAGGAAGTGTGAGTGGAGT 3128
Qy 2360 CCGGGGCTTGTCCAGGATGGCTTCTGTCTGCGCACCAACCCACATCTGTTGAGTTGG 2419
Db 3129 CCGGGGCTTGTCCAGGATGGCTTCTGTCTGCGCACCAACCCACATCTGTTGAGTTGG 3188
Qy 2420 ACCTGACAGGAATGCACCTGAGGATTTGGGCTGAGGTTACTATGCCAGGACTGAGGC 2479
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Db 3249 ACCAGTCTGCAGACTACGCACTTGTGGCTGAAAGATCTGCGGCTCTCACTGCTGCTGCT 3308
Qy 2540 GTGACGAGCTGGGCTCAACTCTCAGTGTGAACAGAGCCTGAGAGAGCTGAGACCTGAGGC 2599
Db 3309 GTGACGAGCTGGGCTCAACTCTCAGTGTGAACAGAGCCTGAGAGAGCTGAGACCTGAGGC 3368
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Db 3429 GCAAGTCCAGACCCCTCGGTTGAGTC 3454

RESULT 13

US-10-162-335-23

; Sequence 23, Application US/10162335

; Publication No. US20040009480A1

; GENERAL INFORMATION:

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; APPLICANT: Baumgartner, Jason C.

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; APPLICANT: Gerlach, Valerie

; APPLICANT: Gorman, Linda

; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Hjalt, Tord

; APPLICANT: Kekuda, Rameeh

; APPLICANT: Li, Li

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Millet, Isabelle

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Patturajan, Meera

; APPLICANT: Rastelli, Luca

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Vernet, Corine A. M.

; APPLICANT: Voos, Edward Z.

; APPLICANT: Zerhusen, Bryan D.

; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Metho

QY 461 GGGGACACGGAGGACCGTGGGACACAGAGCTAGCCCCATCAAGATPAGAGACCCCTTTTG 520
 Db 568 -----AAGACCAAGAGCTGTGAGAGCCCGTGAGTCCCATTAAGATGGAGTTGCTGTTTG 622
 QY 521 AGCCAGACGAGAGCGCCCGAGCAGCCGCGGACCGTGTGATGATGAGAGCGGCGGAGGGA 580
 Db 623 ACCCCGATGATGAGCATTTGAGCCCTGTGCACACCGTGTGTTCAGGGGGCGGAGGGA 682
 QY 581 TAGGCAAGTCCATGCTGGGACACAAAGGTGATGCTGAGCTGGGCGGAGCGGGAAGCTCTTCC 640
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 Db 743 AAGACAGTTTGAATATCTGTCTATATCCATCTGTGCGGAGGTGAGCC---TTGTGACAC 799
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 Db 1460 TCAGGAATCATGGACTGAGAGGGCGGATGTCTGCTTTCTGAGGATGAACCTGTTC 1519
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QY 1521 -----GGCAGGCCAGACCCAGGACGCTGACAGGCTGTGTGACCGAGTACCGCTTTTCTG 1573
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 QY 1574 AAAGGAGCTTCTCGCACTCACAGCCGCTTCTGTTTGGACTCTCTGAAACGAGGAGACCA 1633
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 Db 1760 CCTCTACTTGGAGAGAAATTAAGTTGCAAGATCTCTCAGCAATCAGGCTGGAGCTGC 1819
 QY 1694 TGCACTGATCCAAAGCAAGCTCAGAGCGAGCGCTCCACCTGCGAGAGGGCTCTCTGG 1753
 Db 1820 TGAATGATGAAGTGAAGCCAAAGCTAAAGCTGCAGATCCAGCCAGCAGCTGG 1879
 QY 1754 AGTTCTCAGCTGTGTACGAGATCCAGGAGGAGGATTTATCCAGCAGSCCTGAGCC 1813
 Db 1880 AATGTTCTACTGTTGTACGAGATGCGAGGAGGAGGACTTCGTGCAAGGGCCATGGACT 1939
 QY 1814 ACTTCCAGGTGATCGTGTGTCAGCAATGCTCCAAAGATGGAGCACATGCTCTCTCGT 1873
 Db 1940 ATTTCCCAAGATTGAG---ATCAATCTCTCCACAGATGACCAATGCTTCTTCTCT 1996
 QY 1874 TCTGTCTGAAGCGCTGCGAGGCGCCAGGTGCTGCACTTGTATGGCGCCACCTACAGCG 1933
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 Db 2596 GGAGACTCAGAGTTCGCAATTTTATGTGAAAAAGCAAGAAATCCACAGTGAACCTGCGAG 2655
 QY 2500 ACTTTGTCGCTGAAGTCTCGCCCTCAGTGTGCTGCTGCTGTCAGCAGCTGGGCTCAACT 2559
 Db 2656 AAACCTGGGTGGTGAATTCGTCCTTACGTAGTCTGTGTTTTCAGCTTTGCTCTCGGTA 2715
 QY 2560 CTCAGTGTGAACCAAGAGCCTGAGAGAGCTGGAACCTGAGCCTGTAAGTGTGGGGACCTC 2619

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 15:58:31 ; Search time 8928 Seconds
(without alignments)
13250.868 Million cell updates/sec

Title: US-10-781-294-23
Perfect score: 3108
Sequence: 1 atgtctacgaaccgcaggcag.....atttgacattggtgtgta 3108

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	698	22.5	917	5	BQ920369
3	660.2	21.2	937	5	BQ900330
4	539.8	17.4	571	2	AM673661
5	518.8	16.7	664	9	AG067278
6	494.2	15.9	568	2	AW956628
7	493.8	15.9	669	7	CV030364
8	465.2	15.0	496	8	AQ726243
9	463.8	14.9	499	8	AQ814983
10	426	13.7	764	4	BT911853
11	424.4	13.7	449	8	AQ443134
12	398	12.8	4123	3	HSM000983
13	395	12.7	396	8	AQ094928
14	377	12.1	3359	3	BC021272
15	377	12.1	3360	3	BC012789
16	366.4	11.8	788	4	EM043219
17	354.6	11.4	983	5	BQ710940
18	349.8	11.3	581	9	AG161279
19	343.2	11.0	3475	3	AK087774
20	338.2	10.9	2218	3	AF054176
21	330.8	10.6	643	4	BT519910
22	287.6	9.3	490	9	C6648167
23	282	9.1	496	9	C6663401
24	281	9.0	772	6	CB947742

25	280	9.0	2350	3	CR622836	full-leng
26	276.6	8.9	459	8	AQ716650	HS_5447_B
27	272.6	8.8	1371	9	AY407367	Homo sapi
28	272.6	8.8	1507	3	CR613396	full-leng
29	272.6	8.8	1548	3	CR604056	full-leng
30	272.6	8.8	1612	3	CR592774	full-leng
31	272.6	8.8	1623	3	CR594328	full-leng
32	272.6	8.8	1630	3	CR604995	full-leng
33	272.6	8.8	1647	3	CR606240	full-leng
34	272.6	8.8	1650	3	CR597292	full-leng
35	272.6	8.8	1653	3	CR625171	full-leng
36	272.6	8.8	1657	3	CR590338	full-leng
37	272.6	8.8	1661	3	CR614192	full-leng
38	272.6	8.8	1662	3	CR620826	full-leng
39	272.6	8.8	1664	3	CR600355	full-leng
40	272.6	8.8	1678	3	CR600411	full-leng
41	272.6	8.8	1679	3	CR613915	full-leng
42	272.6	8.8	1680	3	CR624221	full-leng
43	272.6	8.8	1684	3	CR602999	full-leng
44	272.6	8.8	1685	3	CR597816	full-leng
45	272.6	8.8	1687	3	CR608218	full-leng

ALIGNMENTS

RESULT 1
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LOCUS BQ957631 942 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8775651 NIH_MGC_40 Homo sapiens cdna clone IMAGE:6383428
5', mRNA sequence.
ACCESSION BQ957631
VERSION BQ957631.1 GI:22373109
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2576 row: n column: 05
High quality sequence stop: 453.
Location/Qualifiers
1. .942
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6383428"
/issue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 40"
/note="Organ: prostate; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES
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1. .942
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6383428"
/issue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 40"
/note="Organ: prostate; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 24.5%; Score 762.4; DB 5; Length 942;

RESULT 2					
BQ920369					
LOCUS					
DEFINITION	BQ920369	917 bp	mRNA	linear	EST 20-AUG-2002
	AGNCOURT_8918853 NIH_MGC_40 Homo sapiens			cdna clone IMAGE:6383791	
	5' mRNA sequence.				

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Washington University Genome Sequencing Center
 Cloning distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 image.llnl.gov/image/html/iresources.shtml

Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco
 High quality sequence stop: 426.

FEATURES

Location/Qualifiers
 1..571
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone="IMAGE:2900568"
 /cell_line="MGC36"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_10"
 /notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5 kb. Library prepared by Life
 Technologies."

ORIGIN

Query Match 17.4%; Score 539.8; DB 2; Length 571;
 Best Local Similarity 97.7%; Pred. No. 8e-121;
 Matches 558; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
 QY 1297 GGGTTGTGCTCTTGGCGGAGATGGCTCTGAATC-AGAAATCTATTTCAGGAGCA 1355
 Db 571 GGGTTGTGCTGATGCTGGCAGATGGCTCTGAATCAATACCATCTATGTCAGCAGCA 512
 QY 1356 GGACCTCCGGAAGCAGCGCTAGACGGGAAGAGCTCTCTGCCTTCTTCAACATGAACAT 1415
 Db 511 GGACCTCCGGAAGCAGCGCTAGACGGGAAGAGCTCTCTGCCTTCTTCAACATGAACAT 452
 QY 1416 CTTCCAGAGGACATCAACTGTGAGAGTACTACAGCTTCACTTGAAGTTTCAGGA 1475
 Db 451 CTTCCAGAGGACATCAACTGTGAGAGTACTACAGCTTCACTTGAAGTTTCAGGA 392
 QY 1476 ATCTTTGACGATGTACTATATCTTGGACGGGGAGGGGGGCGGAGAGGAGTCT 1535
 Db 391 ATCTTTGACGATGTACTATATCTTGGACGGGGAGGGGGGCGGAGAGGAGTCT 332
 QY 1536 GGACGTGACAGGCTGTGACCGAGTACGGTCTTCTGAAGAGCTTCTGCGCACTCAC 1595
 Db 331 GGACGTGACAGGCTGTGACCGAGTACGGTCTTCTGAAGAGGAGTCTTCTGCGCACTCAC 272
 QY 1596 CAGCGCTTCTGTTTGGACTCTTGAACGAGGAGACGAGGAGCCACCTGGAGAGAGTCT 1655
 Db 271 CAGCGCTTCTGTTTGGACTCTTGAACGAGGAGACGAGGAGCCACCTGGAGAGAGTCT 212
 QY 1656 CTGCTGGAAGGTCTCGCGGACATCAAGATGACCTGTTCAGTGGATCAAAAGCAAAGC 1715
 Db 211 CTGCTGGAAGGTCTCGCGGACATCAAGATGACCTGTTCAGTGGATCAAAAGCAAAGC 152
 QY 1716 TCAGAGCAGCGCTCCACCTGCGAGGAGGCTCTTGGAGTCTTTCAGCTGCTGTACGA 1775
 Db 151 TCAGAGCAGCGCTCCACCTGCGAGGAGGCTCTTGGAGTCTTTCAGCTGCTGTACGA 92
 QY 1776 GATCCAGGAGGAGGAGTATATCCAGAGGCGCTGAGCCACTTCCAGGTGATCGTGGTCAG 1835
 Db 91 GATCCAGGAGGAGGAGTATATCCAGAGGCGCTGAGCCACTTCCAGGTGATCGTGGTCAG 32
 QY 1836 CAACATTCCTCCAGATGGAGCAATGGTC 1866
 Db 31 CAACATTCCTCCAGATGGAGCAATGGTC 1

RESULT 5
 AG067278
 LOCUS

AG067278 664 bp DNA linear GSS 03-NOV-2001

DEFINITION

ACCESSION AG067278.1 GI:16619080
 VERSION AG067278.1
 KEYWORDS Pan troglodytes (chimpanzee)
 SOURCE Pan troglodytes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE BAC end sequences of Library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 664)
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Yokohama, Kanagawa 230-0045, Japan

1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

COMMENT

PRIMERS
 Sequencing: M13Rev

LIBRARY

Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
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 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="PTB-057D11.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

FEATURES

source

ORIGIN

Query Match 16.7%; Score 518.8; DB 9; Length 664;
 Best Local Similarity 92.7%; Pred. No. 1.2e-115;
 Matches 555; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
 QY 750 GCCTCTCCAGGAGCTCATCCGAGTTCCCGAGCGCTCTCTTTTCATCATCGAGGCTTCCA 809
 Db 49 GCATGCTCAGAGCTCATCCGAGTTCCCGAGCGCTCTCTTTTCATCATCGAGGCTTCCA 108
 QY 810 TGAGCTCAAGCTTCTTTTCCAGGATCCTCAGGAGCCCTGCTGCTCTGCTGGAGAGAA 869
 Db 109 TGAGCTCAAGCTTCTTTTCCAGGATCCTCAGGAGCCCTGCTGCTCTGCTGGAGAGAA 168
 QY 870 ACGCCCCACGAGGCTCTCTTAAAGCTTAATTCGGAAGAGCTCTCTCTGAGCTATC 929
 Db 169 ACGCCCCACGAGGCTCTCTTAAAGCTTAATTCGGAAGAGCTCTCTTTTGGAGTATC 258
 QY 930 TTTTGTCTATCACCACAGCGCCACAGCTTTGGAGAGCTCCACCGTCTGCTGGAGCAACC 989
 Db 229 TTTTGTCTATCACCACAGCGCCACAGCTTTGGAGAGCTCCACCGTCTGCTGGAGCAACC 288
 QY 990 CAGGCATGTGGAGATCCTGGGCTTCTCTGAGGAGAAAGGAATATCTTCAAGTA 1049
 Db 289 CAGGCATGTGGAGATCCTGGGCTTCTCTGAGGAGAAAGGAATATCTTCAAGTA 348
 QY 1050 TTTTCCCAATGACAGCAGCGGGCCAGCTCTTCAATTACGTGAGGAGCAACGAGGCTCT 1109
 Db 349 TTTTCCCAATGACAGCAGCGGGCCAGCTCTTCAATTACGTGAGGAGCAACGAGGCTCT 408
 QY 1110 CTTTCCCATGTGCTTGGTCCCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1169
 Db 409 CTTTCCCATGTGCTTGGTCCCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 468


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Qy 1170 GCTGAGGGTGGGGGCTGTTGAGACAGACCTCCAGGACCACTGCACTGTCAGTGTACATGCT 1229
Db 469 GCTGAGGGTGGGGGCTGTTGAGACAGACCTCCAGGACCACTGCGGTGTACATGCT 528
Qy 1230 CTACTCTGTAGTCTGATGCAACCAACCGCGGGGC-CCCGGCTCCAGCCCCCACCACCA 1288
Db 529 CTACTCTGTAGTCTGATGCAACCAACCGCGGGGCCTCAGCCCCCACCACCAACGAAGGT 588
Qy 1289 ACCAGAGAGGTTGTGCTCTTGGCGGAGATGGCTCTGGAATCAGAAAATCTATT 1347
Db 589 TGCANAGAGGTTGTGCTCTTGGCGGAGATGGATCTGGAATCAGAAAATCTATT 647

RESULT 6
LOCUS AW956628 568 bp mRNA linear EST 01-JUN-2000
DEFINITION EST368698 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence.
ACCESSION AW956628
VERSION AW956628.1 GI:8146311
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 568)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: john@tigr.org
Plate: 94
Seq primer: Reverse.
FEATURES
source Location/Qualifiers
1..568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGD"
/note="Vector: pbluescriptSKm"
ORIGIN
Query Match 15.9%; Score 494.2; DB 2; Length 568;
Best Local Similarity 97.4%; Pred. NO. 1.2e-109;
Matches 523; Conservative 0; Mismatches 10; Indels 4; Gaps 2;
Qy 1638 CCACCTGGAGAGAGTCTCTCTGGAAGGTTCGCGGCACATCAAGATGGACCTGTGCA 1697
Db 1 CCACCTGGAGAGAGTCTCTCTGGAAGGTTCGCGGCACATCAAGATGGACCTGTGCA 60
Qy 1698 GTGATCCAAAGCAAGCTCAGAGCGAGCGGTCCACCTGCAGCAGGCTCTCTTGGAGTT 1757
Db 61 GTGATCCAAAGCAAGCTCAGAGCGAGCGGTCCACCTGCAGCAGGCTCTCTTGGAGTT 120
Qy 1758 CTTGAGTCTGTGACGAGATCCAGGAGGAGGTTTATCCAGCAGGCGCTGAGCCACTT 1817
Db 121 CTTGAGTCTGTGACGAGATCCAGGAGGAGGTTTATCCAGCAGGCGCTGAGCCACTT 180
Qy 1818 CCAGTGTATCTGCTCAGCAACATTCCTCAAGATGAGACATGTCCTCTCTGTCG 1877
Db 181 CCAGTGTATCTGCTCAGCAACATTCCTCAAGATGAGACATGTCCTCTCTGTCG 240
Qy 1878 TCTGAAGCGCTGAGGAGCGCCAGGTGCTGACCTTGTATGCGCGCACCTACAGCGGGA 1937
Db 241 TCTGAAGCGCTGAGGAGCGCCAGGTGCTGACCTTGTATGCGCGCACCTACAGCGGGA 300

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Qy 1938 CGGGGAAGACCGCGCAGGTGCTCCGAGGAGCCACACACGCTTGTGTCAGCTCAGACC 1997
Db 301 CGGGGAAGACCGCGCAGGTGCTCCGAGGAGCCACACACGCTTGTGTCAGCT---ACC 357
Qy 1998 AGAGAGACCGTCTCTGTCGACCGCTACAGTGAACATCTGCAGCGGCCCTGTGCACCAA 2057
Db 358 AGAGAGACCGTCTCTGTCGACCGCTACAGTGAACATCTGCAGCGGCCCTGTGCACCAA 417
Qy 2058 TCCAAACCTGATAGAGCTGCTCTGTACCCGAAATGCGCTGGCGAGCGCGGGGTGAAGCT 2117
Db 418 TCCAAACCTGATAGAGCTGCTCTGTACCCGAAATGCGCTGGCGAGCGCGGGGTGAAGCT 477
Qy 2118 GCTCTGTCAAGACTCAGACACCCCAACTGCAAACTTCAGAACTCGAGGCTGAAGAG 2174
Db 478 GCTCTGTCAAGACTCAGACACCCCAACTGCAAACTTCAGAA-CTGAGGCTGGAGAG 533

RESULT 7
LOCUS CV030364 669 bp mRNA linear EST 20-AUG-2004
DEFINITION 9461 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC028069, mRNA sequence.
ACCESSION CV030364
VERSION CV030364.1 GI:51488613
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 669)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerre,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenhaute,J., Cusick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M.
Human ORFeome Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGCTACGAACCGCAGGCAG
BACKWARD: CAGCAGCCAATGTCCAAA
Insert Length: 669 Std Error: 69.00
Plate: 11079 row: 09 column: F
Seq primer: ACTGGCGTGTTCACACGTCGTGACTGGGAAAC
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High quality sequence stop: 668
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/tissue_type="mixed"
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/note="Vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor vector. Reference : MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"
ORIGIN

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RESULT 9
AQ814983
LOCUS
DEFINITION
  AQ814983 499 bp DNA linear GSS 25-AUG-1999
  HS 5249 B2 G05 SP6E RPCI-11 Human Male BAC Library Homo sapiens
  genomic_clone Plate=825 Col=10 Row=N, genomic survey sequence.
ACCESSION
  AQ814983
SOURCE
  AQ814983.1 GI:5775961
KEYWORDS
  GSS.
ORGANISM
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 499)
  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
  Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  99380589
  10449764
COMMENT
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
  or from Resear h Genetics (info@resgen.com). BAC end Web Server:
  http://www.htsc.washington.edu
  Plate: 825 Row: N Column: 10
  Seq primer: SP6
  Class: BAC ends
  High quality sequence stop: 499.
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      Male blood DNA was isolated from one randomly chosen donor
      and partially digested with a combination of EcoRI and
      EcoRI Methylase. Size selected DNA was cloned into the
      pBACe3.6 vector at EcoRI sites"
FEATURES
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    1..499
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      /clone_lib="NIH MGC 118"
      /notes="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
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      and directionally cloned (EcoRV site is destroyed upon
      cloning). Average insert size 1.7 kb, insert size range
      1.2-3.3 kb. Library is normalized and enriched for
      full-length clones and was constructed by C. Gruber
      (invitrogen). Research Genetics tracking code 027. Note:
      this is a NIH_MGC Library."
ORIGIN
  Query Match 13.7%; Score 426; DB 4; Length 764;
  Best Local Similarity 86.7%; Pred. No. 6.5e-93;
  Matches 539; Conservative 0; Mismatches 0; Indels 83; Gaps 3;

1720 AGGACGGCTCCACCCCTGCAGCAGGGCTCCTTGGAGTTCTTTCAGCTGCTTGTACGAGATC 1779
    |||||
241 AGGCACGGCTCCACCCCTGCAGCAGGGCTCCTTGGAGTTCTTTCAGCTGCTTGTACGAGATC 300
    |||||
1780 CAGGAGGAGGAGTTTATCCAGCAGCGCCCTCGAGCCACTTCCAGGTGATCGTGGTTCAGCAAC 1839
    |||||
301 CAGGAGGAGGAGTNTATCCAGCAGCGCCCTCGAGCCACTTCCAGGTGATCGTGGTTCAGCAAC 360
    |||||
1840 ATTGCCTCCCAAGATGGAGCACATGGTCTCCTCGTTCTGTCTGAAGCGCTGCAGAGCGCC 1899
    |||||
361 ATTGCCTTCAAGATGGAGCACATNGTCTCCTCGTCTGTCTGAAGCGCTGCAGAGCGCC 420
    |||||
1900 CAGGTGCTGCATTGTATGGCGCACCTACAGCGCGACCGGGGAAGACCGCGCGAGGTGC 1959
    |||||
421 CAGGTGCTGCATTGTATGGCGCACCTACAGCGCGACCGGGGAAGACCGCGCGAGGTGC 480
    |||||
1960 TCCGACGAGGCGCACAC 1976
    |||||
481 TCTCGATGATCGCACAC 497
    |||||

RESULT 10
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LOCUS
DEFINITION
  BI911853 603063634f1 NIH_MGC_118 Homo sapiens cdna clone IMAGE:5212737 5',
  mRNA sequence.
ACCESSION
  BI911853
KEYWORDS
  BI911853.1 GI:16175736
  EST.
SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 764)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Life Technologies, Inc.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM11534 Row: C Column: 10
  High quality sequence start: 22
  High quality sequence stop: 764.
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      /notes="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
      non-activated adult donors. Library is oligo-dT primed
      and directionally cloned (EcoRV site is destroyed upon
      cloning). Average insert size 1.7 kb, insert size range
      1.2-3.3 kb. Library is normalized and enriched for
      full-length clones and was constructed by C. Gruber
      (invitrogen). Research Genetics tracking code 027. Note:
      this is a NIH_MGC Library."
ORIGIN
  Query Match 13.7%; Score 426; DB 4; Length 764;
  Best Local Similarity 86.7%; Pred. No. 6.5e-93;
  Matches 539; Conservative 0; Mismatches 0; Indels 83; Gaps 3;

```


REFERENCE
AUTHORS
CONSRW
TITLE
JOURNAL

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 4123)
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fob, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the
Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZ58601822) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZ58601822
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES
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gene
CDS

ORIGIN

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VERSION
A0094928.1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

1 (bases 1 to 396)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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FEATURES
source

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Db 61 GCTTCTCTGTTTGGACTCTCTGAACGAGGAGACACGAGCCACCTGGAGAGAGTCTCTGT 120

Qy 1661 GGAAGTCTTCGCGCACATCAAGATGGAACCTTTGAGTGGATCCAAAGCAAGTCTAGA 1720

Db 121 GGAAGTCTTCGCGCACATCAAGATGGAACCTTTGAGTGGATCCAAAGCAAGTCTAGA 180

Qy 1721 GCGACGGCTCCACCTTCGACGAGGCTCCTTCGAGTCTTTCAGTCTGTTGTAGAGATCC 1780

Db 181 GCGACGGCTCCACCTTCGACGAGGCTCCTTCGAGTCTTTCAGTCTGTTGTAGAGATCC 240

Qy 1781 AGGAGGAGGAGTTTATCCAGCAGGCGCTCAGCCACTTCAGGTGATTCGTTGTCAGCA 1840

Db 241 AGGAGGAGGAGTTTATCCAGCAGGCGCTCAGCCACTTCAGGTGATTCGTTGTCAGCA 300

Qy 1841 TTGCTCTCAAGATGGAAGCAGATGGTCTCCTGTTCTGTTCTGAGCGCTCAGAGAGCGCC 1900

Db 301 TTGCTCTCAAGATGGAAGCAGATGGTCTCCTGTTCTGTTCTGAGCGCTCAGAGAGCGCC 360

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Db 361 AGGTGCTGCACTTGTATGGCGCCACCTACAGCGCGG 396

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HTC.

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BC021272
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SOURCE	Homo sapiens (human)	Query Match	12.1%; Score 377; DB 3; Length 3359;
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REFERENCE	1. (bases 1 to 3359)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullighy, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.F., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2. (bases 1 to 3359)		
AUTHORS	Director MGC Project.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	On Aug 19, 2003 this sequence version replaced gi:18204229. Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisec.nih.gov/ Contact: nisc.mgc@nih.gov Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Loric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Toungeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.		
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 3360)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Utsid,T.B., Toshiyuki,S., Carninci,P., Prange,C., Roha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richardson,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Small,D.B., Schnurch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 JOURNAL
 PUBMED
 REFERENCE 2 (bases 1 to 3360)
 DIRECTOR MGC Project.
 AUTHORS
 TITLE Direct Submission

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OM protein - protein search, using sw model

Run on: February 8, 2005, 14:41:04 ; Search time 173 Seconds
(without alignments)
2313.855 Million cell updates/sec

Title: US-10-781-294-24

Perfect score: 5472

Sequence: 1 MLRTAGRDGLCRSLTYLEEL.....MTHSRLLAALRVTPYLDIGC 1035

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5472	100.0	1035	5 ADE36417	Ad36417 Human PAA
2	5472	100.0	1035	8 ADJ19339	Adj19339 Human PAN
3	5448.5	99.6	1062	8 ADP47724	Adp47724 Human Mon
4	5433	99.3	1061	5 AAO15590	Aao15590 Human PYR
5	5433	99.3	1061	7 ADF94755	Adf94755 Human PYR
6	5389	98.5	1099	5 AAO17857	Aao17857 Pyrin dom
7	5259.5	96.1	1027	8 ADJ19383	Adj19383 Human PAN
8	5113.5	93.4	1006	8 ADP47726	Adp47726 Human Mon
9	5077.5	92.8	1004	7 ADM04476	Adm04476 Human pro
10	4799.5	87.7	950	8 ADP47728	Adp47728 Human Mon
11	4520	82.6	865	7 ADC31287	Adc31287 Human nov
12	4458.5	81.5	892	8 ADP47730	Adp47730 Human Mon
13	3996	73.0	1033	8 ADP47732	Adp47732 Murine Mo
14	3364	61.5	635	8 ADJ19399	Adj19399 Human PAN
15	3163	57.8	603	5 ADE36457	Ad36457 Human PAN
16	3163	57.8	603	8 ADJ19379	Adj19379 Human PAN
17	3005	54.9	582	6 ABU99119	Abu99119 Novel hum
18	3005	54.9	582	8 ADM93803	Adm93803 Human NOV
19	2953.5	54.0	565	5 ABG97475	Abg97475 Human nuc
20	2694.5	49.2	521	6 ABU99120	Abu99120 Novel hum
21	2671.5	48.8	521	8 ADM93805	Adm93805 Human NOV
22	2513	45.9	472	8 ADP47884	Adp47884 Human CAT
23	2396	43.8	1034	4 AAE07514	Aae07514 Human PYR
24	2396	43.8	1034	4 ABU08503	Abu08503 Huma PYR
25	2396	43.8	1034	6 ABU63315	Abu63315 Human pyr

ALIGNMENTS

RESULT 1

ADE36417

ID ADE36417 standard; protein; 1035 AA.

XX AC ADE36417;

XX DT 29-JAN-2004 (first entry)

XX DE Human PAAD and nucleotide binding protein PAN6.

XX KW cytostatic; immunosuppressive; vulnary; antiinflammatory; vasotropic;
KW antiallergic; antitumor; dermatological; cerebroprotective; cardiant;
KW antiparkinsonian; neurotropic; neuroprotective; anti-HIV; gene therapy;
KW NF-kappaB activation inhibitor; PAAD domain containing polypeptide;
KW PAAD and nucleotide binding protein 2-6; PAN 2-6; pyrin 2;
KW apoptosis-associated spect-like protein; caspase recruitment domain 2;
KW ASC-2; nuclear factor kappa B activation inhibitor; NB-ARC domain;
KW apoptosis; NF-kappaB induction; cytokine processing;
KW cytokine receptor signaling caspase-mediated proteolysis;
KW c-Jun N-terminal kinase activation; cell life; cell death; apoptosis;
KW inflammation; cell adhesion; cancer; keratinocyte; hyperplasia;
KW neoplasia; keloid benign prostatic hypertrophy; inflammatory hyperplasia;
KW fibrosis; smooth muscle cell proliferation; balloon angioplasty;
KW restenosis; leukaemia; lymphoma; inflammatory disease; allergy;
KW arthritis; lupus; schrojen's syndrome; Crohn's disease;
KW ulcerative colitis; graft versus host disease; stroke; heart failure;
KW neurodegenerative disease; parkinson's disease; Alzheimer's disease; HIV;
KW cancer therapy; PAAD domain family; human; PAN6.

XX OS Homo sapiens.

XX US US2003077699-A1.

XX PD 24-APR-2003.

XX PF 25-SEP-2001; 2001US-00965621.

XX PR 26-SEP-2000; 2000US-00671760.

XX PR 26-SEP-2000; 2000US-0367367P.

XX PA (REED//) REED J C.

XX PA (GODZ//) GODZIK A.

XX PA (CHUZ//) CHU Z.

XX PA (PAWL//) PAWLOWSKI K.

XX PA (FIOR//) FIORENTINO L.

XX PA (ARIZ//) ARIZA M E.

XX PA (STEH//) STEHLIK C.

XX XX

PI Reed JC, Godzik A, Chu Z, Pawlowski K, Fiorentino L, Ariza ME;
PI Stehlik C;
XX
XX WPI: 2002-471256/50.
DR N-PSDB; ADE36416.
XX
XX Novel isolated PAAD domain containing polypeptide useful for inducing
PT apoptosis by inhibiting nuclear factor kappa B activation and in gene
PT therapy for treating cancer.
XX
XX Claim 18; SEQ ID NO 24; 93pp; English.
XX
XX The invention describes an isolated PAAD domain containing polypeptide
CC (I) comprising 80% identity to the amino acid sequence of PAAD and
CC nucleotide binding protein (PAN) 2-6, pyrin 2, apoptosis-associated speck
CC -like protein containing a caspase recruitment domain (ASC)-2 fully
CC defined in specification, where (I) is biologically active. (I) is useful
CC for identifying a (I)-associated polypeptide, an agent altering that
CC association and agents that modulate PAAD domain mediated inhibition of
CC nuclear factor kappa B (NF-kappaB). A NB-ARC domain polypeptide is useful
CC for identifying an agent that modulates the activity of the NB-ARC domain
CC of (I). (I) or its functional fragments is useful in altering cellular or
CC biochemical process such as apoptosis, NF-kappaB induction, cytokine
CC processing, cytokine receptor signaling caspase-mediated proteolysis or c
CC -Jun N-terminal kinase activation, thus having modulating effect on cell
CC life and death (apoptosis) inflammation, cell adhesion or other cellular
CC or biochemical processes. (I) is useful for treating cancer pathologies,
CC keratinocyte, hyperplasia, neoplasia, keloid benign prostatic
CC hypertrophy, inflammatory hyperplasia, fibrosis, smooth muscle cell
CC proliferation in arteries following balloon angioplasty (restenosis),
CC leukemia, lymphomas; inflammatory diseases such as allergies, arthritis,
CC lupus, schroten's syndrome, Crohn's disease and ulcerative colitis, graft
CC versus host disease, stroke, heart failure, neurodegenerative diseases
CC such as parkinson's and Alzheimer's disease, human immunodeficiency virus
CC infection (HIV). (I) is useful for diagnosing cancer or monitoring cancer
CC therapy. This is the amino acid sequence of a human PAAD and nucleotide
CC binding protein PAN6.
XX
XX Sequence 1035 AA;
SQ Query Match 100.0%; Score 5472; DB 5; Length 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRTAGDGLCRSLTYLBEAVALKPKFLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
DB 1 MLRTAGDGLCRSLTYLBEAVALKPKFLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
QY 61 ITHFGPEAWRLALSTFERINRKLWEGQREDLVRDPOETRYDYVRKFKRLMEDRNARL 120
DB 61 ITHFGPEAWRLALSTFERINRKLWEGQREDLVRDPOETRYDYVRKFKRLMEDRNARL 120
QY 121 GECVNLSHRYTRLLLVKHSNPMVQQLDGTGRGHARTVGHQASPIKIETLFPDDEBP 180
DB 121 GECVNLSHRYTRLLLVKHSNPMVQQLDGTGRGHARTVGHQASPIKIETLFPDDEBP 180
QY 181 EPPRTVMQGAAGIGKSMALAHKVMLDWADGKLFQGRDYLYFYNCREMNQATSCSMQDL 240
DB 181 EPPRTVMQGAAGIGKSMALAHKVMLDWADGKLFQGRDYLYFYNCREMNQATSCSMQDL 240
QY 241 IFSCWPEPSAPLQELIRVERPRLFFIDGFDLKPSPHDPQGPWCILCWEKRPTELLNSL 300
DB 241 IFSCWPEPSAPLQELIRVERPRLFFIDGFDLKPSPHDPQGPWCILCWEKRPTELLNSL 300
QY 301 IRKLLPELSLITTRPTALEKHLLEHPRHVEILGFSEARKEFYKYFHNAEQAOV 360
DB 301 IRKLLPELSLITTRPTALEKHLLEHPRHVEILGFSEARKEFYKYFHNAEQAOV 360
QY 361 FNVVRNEPLFTWCFVPLVCVVCTCQQQLSGGLLROTSRTTAVYMLYLLSLMQPKP 420
DB 361 FNVVRNEPLFTWCFVPLVCVVCTCQQQLSGGLLROTSRTTAVYMLYLLSLMQPKP 420
QY 421 GAPRLQPPPNQRLCSLAADGLMNQKILFEEQDLRKHGDLGSDVSAFLNMNIFQKDINCE 480

DB 421 GAPRLQPPPNQRLCSLAADGLMNQKILFEEQDLRKHGDLGSDVSAFLNMNIFQKDINCE 480
QY 481 RYYSFIHLSFOEPFAAMYIILDEGEGGAGPDQDVTLLITYAFSERSFLATLSRFLGLL 540
DB 481 RYYSFIHLSFOEPFAAMYIILDEGEGGAGPDQDVTLLITYAFSERSFLATLSRFLGLL 540
QY 541 NEETRSHLEKSLCWKSPHVKMDLQWIOSKAQSDGSTLQOQSGSLFEFFSCLYEIQEEFFIQ 600
DB 541 NEETRSHLEKSLCWKSPHVKMDLQWIOSKAQSDGSTLQOQSGSLFEFFSCLYEIQEEFFIQ 600
QY 601 QALSHFOVIVYSNIASKMEHVSFCLKRCRSQAQVLLHYGATYSADGEDRARCAGAHLL 660
DB 601 QALSHFOVIVYSNIASKMEHVSFCLKRCRSQAQVLLHYGATYSADGEDRARCAGAHLL 660
QY 661 LVQLRPERTVLLDAYSEHAAALCTNPNLIELSYRNALGSRGVKLLCOGLRHNPCKLQ 720
DB 661 LVQLRPERTVLLDAYSEHAAALCTNPNLIELSYRNALGSRGVKLLCOGLRHNPCKLQ 720
QY 721 LRLKCRISSSACEDLSAALIANKNLITMDLSGNGVGPFGMMLLCEGLRHPQCRLOMIQL 780
DB 721 LRLKCRISSSACEDLSAALIANKNLITMDLSGNGVGPFGMMLLCEGLRHPQCRLOMIQL 780
QY 781 RKQLESAGCQEMASVLTGNPHLVELDITGNALDELGLRLCEGLRHPVCELRITLWKIC 840
DB 781 RKQLESAGCQEMASVLTGNPHLVELDITGNALDELGLRLCEGLRHPVCELRITLWKIC 840
QY 841 RUTAAACDELASTLSVNSQSLRELDLSNELGDLVLLCEGLRHPTCKLQTLRLGICRLG 900
DB 841 RUTAAACDELASTLSVNSQSLRELDLSNELGDLVLLCEGLRHPTCKLQTLRLGICRLG 900
QY 901 SAACGLSVLVQANHNRELDLSFNDLGDWGLWLLAEGLQHPACRLQKMLDSCGLTAKA 960
DB 901 SAACGLSVLVQANHNRELDLSFNDLGDWGLWLLAEGLQHPACRLQKMLDSCGLTAKA 960
QY 961 CENLYFTLGINTLTDLYLTNNALGDTGVRLCKELSHPGCKLRVWLFGMDLNKWTSHR 1020
DB 961 CENLYFTLGINTLTDLYLTNNALGDTGVRLCKELSHPGCKLRVWLFGMDLNKWTSHR 1020
QY 1021 LAALRVTKPYLDIGC 1035
DB 1021 LAALRVTKPYLDIGC 1035
RESULT 2
ADJ19339
ID ADJ19339 standard; protein; 1035 AA.
XX AC ADJ19339;
XX DT 20-MAY-2004 (first entry)
XX DE Human PAN6 PAAD domain-containing full-length protein.
XX KW PAAD; cytostatic; cancer; gene therapy; PAAD domain; human; PAN6.
XX OS Homo sapiens.
XX PN US2004002593-A1.
XX PD 01-JAN-2004.
XX PF 04-APR-2003; 2003US-00407866.
XX PR 04-APR-2002; 2002US-0370538P.
XX PA (REED/) REED J C.
XX FA (GODZ/) GODZIK A.
XX PI Reed JC, Godzik A;
XX WPI: 2004-061677/06.
XX N-PSDB; ADJ19338.

QV	934	LLAEGLOHPACRLQKWLWDSCLTKAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC	993		Matches 1034;	Conservative	0;	Mismatches	0;	indels	20;	gaps
QV	934	LLAEGLOHPACRLQKWLWDSCLTKAKACENLYFTLGINQTLTDLTYLTNNALGDTGVRLLC	993		Matches 1034;	Conservative	0;	Mismatches	0;	indels	20;	gaps

Best Local Similarity	2.147	2.147	2.147	2.147
Mismatches	0	0	0	0
Indels	0	0	0	0
Gaps	0	0	0	0

Qy 1 MLRTAGDGLCRSLTYLSEELBAVELKKFKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
Db 1 MLRTAGDGLCRSLTYLSEELBAVELKKFKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
Qy 61 ITHFGPEEAWRLALSTFERINRKLWEGQREDLVR----- 96
Db 61 ITHFGPEEAWRLALSTFERINRKLWEGQREDLVR----- 120
Qy 97 ---DPQETRYDYVRKFRMLMDRNLARLGEVNLSHRYTRLLLVKEHSPNMQVQQQLDGTG 153
Db 121 PRKDPQETRYDYVRKFRMLMDRNLARLGEVNLSHRYTRLLLVKEHSPNMQVQQQLDGTG 180
Qy 154 RGHARTVGHQASPIKIETLFPDDEERPPPTVVMQGAAGTCKSLAHKVMLDWADGKLF 213
Db 181 RGHARTVGHQASPIKIETLFPDDEERPPPTVVMQGAAGTCKSLAHKVMLDWADGKLF 240
Qy 214 QGRDYLFIYINCREMNQATSCSQDILFSCWPEPSAPLOELIRVPERLLFIIDGPELK 273
Db 241 QGRDYLFIYINCREMNQATSCSQDILFSCWPEPSAPLOELIRVPERLLFIIDGPELK 300
Qy 274 PSFHDPOQPWCLCWEKRPTELLNSLRKLLPELSLITRPTALEKHLRLLEHPRHV 333
Db 301 PSFHDPOQPWCLCWEKRPTELLNSLRKLLPELSLITRPTALEKHLRLLEHPRHV 360
Qy 334 EILGFSEARKEYFYKYFHNAEQAGQVFNVDNEPLFTMCFVPLVCWVCTCLQQOLEG 393
Db 361 EILGFSEARKEYFYKYFHNAEQAGQVFNVDNEPLFTMCFVPLVCWVCTCLQQOLEG 420
Qy 394 GGLLRQTSRTTAVMYLLSLMOPKPGAPLQPPNQRLGCLSAADGLMNQKILFBEQD 453
Db 421 GGLLRQTSRTTAVMYLLSLMOPKPGAPLQPPNQRLGCLSAADGLMNQKILFBEQD 480
Qy 454 LRKGLDGEDVSALFNWNI FOKDNCERYYFIHLSPQEPFAAMYIILDEGEGAGDQD 513
Db 481 LRKGLDGEDVSALFNWNI FOKDNCERYYFIHLSPQEPFAAMYIILDEGEGAGDQD 540
Qy 514 VTRLLTEYAFSERSFLALTSLRFLGLNEETRSLEKSLCKVSPHIMDLLOWIQSKAQ 573
Db 541 VTRLLTEYAFSERSFLALTSLRFLGLNEETRSLEKSLCKVSPHIMDLLOWIQSKAQ 600
Qy 574 SDGSTLOQSLSEFFSCLYEIEBEFFIQALSHFQVIVVNSIASQVHEWVSFCLKCRSA 633
Db 601 SDGSTLOQSLSEFFSCLYEIEBEFFIQALSHFQVIVVNSIASQVHEWVSFCLKCRSA 660
Qy 634 QVLHLYGATYSADGEDRARCAGAHLLVQLRPTVLLDAYSEHLAAALCTNPNLIELS 693
Db 661 QVLHLYGATYSADGEDRARCAGAHLLVQLRPTVLLDAYSEHLAAALCTNPNLIELS 719
Qy 694 LYRNALGSRGVKLLCQGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 753
Db 720 LYRNALGSRGVKLLCQGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 779
Qy 754 NGVFPQGMMLICEGLRHQPQRLQWQRLKQLESGACQEMASVLTGTPHVLVELDTGNAL 813
Db 780 NGVFPQGMMLICEGLRHQPQRLQWQRLKQLESGACQEMASVLTGTPHVLVELDTGNAL 839
Qy 814 EDLGLRLCCQGLRHPVCLRTLWLKICRLTAAACDELASTLSVNSQSLRELDLSLNEIGDL 873
Db 840 EDLGLRLCCQGLRHPVCLRTLWLKICRLTAAACDELASTLSVNSQSLRELDLSLNEIGDL 899
Qy 874 GVLLICEGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRLDELDFNDLGDWGLW 933
Db 900 GVLLICEGLRHPTCKLQTLRLGICRLGSAACEGLSVVLQANHNRLDELDFNDLGDWGLW 959
Qy 934 LLAEGLOHPACRLQKMLDSCGLTAKACENIYFTLGINQTLTDLYLTNNALGDTGVRLLC 993
Db 960 LLAEGLOHPACRLQKMLDSCGLTAKACENIYFTLGINQTLTDLYLTNNALGDTGVRLLC 1019
Qy 994 KRLSHPGCKRLVLMFGMDLNKMTHSRLAALRVTKPYLDIGC 1035
Db 1020 KRLSHPGCKRLVLMFGMDLNKMTHSRLAALRVTKPYLDIGC 1061

RESULT 5
ADF94755
ID ADF94755 standard; protein; 1061 AA.
XX
AC ADF94755;
XX
DT 26-FEB-2004 (first entry)
XX
DB Human PYRIN-8 protein #2.
XX
KW human; PYRIN; inflammatory disorder; inappropriate apoptosis;
KW inflammatory bowel disease; rheumatoid arthritis; diabetes;
KW multiple sclerosis; Grave's disease; contact dermatitis; psoriasis;
KW graft rejection; asthma; allergy; chronic obstructive pulmonary disease;
KW glomerulonephritis; infection; Alzheimer's disease; Parkinson's disease;
KW anaemia; ischaemia; screening; chromosomal mapping; tissue typing;
KW forensic biology; pharmacogenomics; predictive medicine.
XX
OS Homo sapiens.
XX
PN WO2003089588-A2.
XX
PD 30-OCT-2003.
XX
PF 14-APR-2003; 2003WO-US011572.
XX
PR 17-APR-2002; 2002US-00124498.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PA (AMHP) WYETH.
XX
PI Bertin J, Wang W, Blatcher M;
XX
DR WPI; 2003-845527/78.
DR N-PSDB; ADF94754.
XX
New nucleic acid molecules and polypeptides (e.g. PYRIN-2 or PYRIN-3)
PT useful for diagnosing, preventing or treating inflammation or disorders
PT associated with inappropriate apoptosis, in chromosomal mapping or in
PT pharmacogenomics.
XX
PS Claim 8; SEQ ID NO 18; 199pp; English.
XX
The invention comprises the amino acid and coding sequences of human
CC PYRIN proteins. The DNA and protein sequences of the invention are useful
CC in diagnosing, preventing and treating inflammatory disorders or
CC disorders associated with inappropriate apoptosis, such as: inflammatory
CC bowel disease, rheumatoid arthritis, diabetes, multiple sclerosis,
CC Grave's disease, contact dermatitis, psoriasis, graft rejection, asthma,
CC allergy, chronic obstructive pulmonary disease, glomerulonephritis,
CC infections, Alzheimer's disease, Parkinson's disease, anaemia and
CC ischaemia. The DNA and protein sequences of the invention may also be
CC used in screening assays, chromosomal mapping, tissue typing, forensic
CC biology, pharmacogenomics, predictive medicine, and in monitoring of
CC clinical trials. The present amino acid sequence represents a PYRIN
CC protein of the invention.
XX
SQ Sequence 1061 AA;

Query Match 99.3%; Score 5433; DB 7; Length 1061;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1034; Conservative 0; Mismatches 0; Indels 28; Gaps 2;
Qy 1 MLRTAGDGLCRSLTYLSEELBAVELKKFKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
Db 1 MLRTAGDGLCRSLTYLSEELBAVELKKFKLYLTATLGECKIPWGSMEKAGPLEMAQLL 60
Qy 61 ITHFGPEEAWRLALSTFERINRKLWEGQREDLVR----- 96
Db 61 ITHFGPEEAWRLALSTFERINRKLWEGQREDLVR----- 120
Qy 97 ---DPQETRYDYVRKFRMLMDRNLARLGEVNLSHRYTRLLLVKEHSPNMQVQQQLDGTG 153

QY 361 FNYVRDNEPLFTMCFVPLVWVCTCLOQQLGGGLLRQTSRTTTAVYMLYLLSLMQPKP 420
Db |||||
QY 361 FNYVRDNEPLFTMCFVPLVWVCTCLOQQLGGGLLRQTSRTTTAVYMLYLLSLMQPKP 420
Db |||||
QY 421 GAPRLQPPNORGICSLAAGLWQKILFEQDLRKXGLDGEDVSFAFLNMNIFQKDINCE 480
Db |||||
QY 421 GAPRLQPPNORGICSLAAGLWQKILFEQDLRKXGLDGEDVSFAFLNMNIFQKDINCE 480
Db |||||
QY 481 RYYSFIHLSFOEFAAAYIILDEGEAGAGPQDVTRLLITEYAFSERSFLALTSRFLGCLL 540
Db |||||
QY 481 RYYSFIHLSFOEFAAAYIILDEGEAGAGPQDVTRLLITEYAFSERSFLALTSRFLGCLL 540
Db |||||
QY 541 NEETRSHLEKSLCWKVSPIHMDLQWTSQAQSDGSTLQOQSLFFSCLYEIQEEBFQ 600
Db |||||
QY 541 NEETRSHLEKSLCWKVSPIHMDLQWTSQAQSDGSTLQOQSLFFSCLYEIQEEBFQ 600
Db |||||
QY 601 QALSHFOVIVVSNIAKMEHVMVSFCLKRCRCSAQLVHLGYATYSADGEDRARCAGATL 660
Db |||||
QY 601 QALSHFOVIVVSNIAKMEHVMVSFCLKRCRCSAQLVHLGYATYSADGEDRARCAGATL 660
Db |||||
QY 661 LVQLRPERTVLLDAYSEHLAAALCTPNLIELSLYRNALSGRGVKKLLCOGLRHPNCKLQN 720
Db |||||
QY 661 LVQLRPERTVLLDAYSEHLAAALCTPNLIELSLYRNALSGRGVKKLLCOGLRHPNCKLQN 720
Db |||||
QY 721 LRLKCRISACBDLSAALIANKNLITRMDLSGNGVGPFGMWLLCEGLRHPQCRLOMIQL 780
Db |||||
QY 721 LRLKCRISACBDLSAALIANKNLITRMDLSGNGVGPFGMWLLCEGLRHPQCRLOMIQL 780
Db |||||
QY 781 RKCOLESACQEMASVLGTNPHLVELDTGNALDELGLRLCOGLRHPVCELRITLWLKIC 840
Db |||||
QY 781 RKCOLESACQEMASVLGTNPHLVELDTGNALDELGLRLCOGLRHPVCELRITLWLKIC 840
Db |||||
QY 841 RLTAACDELASTLSVNQSLRELDLSNELDGLVLLICEGLRHPCTCKLQTLRLGICRLG 900
Db |||||
QY 841 RLTAACDELASTLSVNQSLRELDLSNELDGLVLLICEGLRHPCTCKLQTLRLGICRLG 900
Db |||||
QY 901 SAACEGLSVLQANHNRELDLSFNDLGDWGLWLLAEGLOHPACRLQKLMWDSGLTAKA 960
Db |||||
QY 901 SAACEGLSVLQANHNRELDLSFNDLGDWGLWLLAEGLOHPACRLQKLMWDSGLTAKA 960
Db |||||
QY 961 CENLYFTLGINQTLTDLYLTNNALGDTGVRLLCRLSHPGCKLRVLMFGMDLNKMTHS 1019
Db |||||
QY 961 CENLYFTLGINQTLTDLYLTNNALGDTGVRLLCRLSHPGCKLRVLMFGMDLNKMTHS 1019
Db |||||

RESULT 7

ADJ19383
ID ADJ19383 standard; protein; 1027 AA.
XX
AC
XX
XX
DT 20-MAY-2004 (first entry)
XX
DE Human PAN6 PAAD domain-containing full-length protein 2.
XX
KW PAAD; cytostatic; cancer; gene therapy; human; PAAD domain; PAN6.
XX
OS Homo sapiens.
XX
FN US2004002593-A1.
XX
PD 01-JAN-2004.
XX
PF 04-APR-2003; 2003US-00407866.
XX
PR 04-APR-2002; 2002US-0370538P.
XX
PA (REED/) REED J C.
PA (GODZ/) GODZIK A.
XX
PI Reed JC, Godzik A;
XX
XX WPI; 2004-061677/06.
DR

DR N-PSDB; ADJ19382.
XX
PT New nucleic acid molecule encoding a PAAD-containing polypeptide, useful
PT for preparing a composition for diagnosing or treating e.g., cancer.
XX
PS Claim 14; SEQ ID NO 68; 193pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule encoding
CC a PAAD-containing polypeptide. The polypeptide of the invention
CC demonstrates cytostatic activity and may be useful for preparing a
CC composition for diagnosing or treating diseases associated with the PAAD
CC domain-containing polypeptide, such as cancer, via gene therapy. The
CC current sequence is that of the human PAAD domain-containing full-length
CC protein of the invention.
XX
SQ Sequence 1027 AA;

Query Match 36.1%; Score 5259.5; DB 8; Length 1027;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 MLRTAGRDGLCRSLSTYLEEAEVLEKFKLYLGTATLGEKIPWGSMEKAGPLEMAQLL 60
Db |||||
QY 1 MLRTAGRDGLCRSLSTYLEEAEVLEKFKLYLGTATLGEKIPWGSMEKAGPLEMAQLL 60
Db |||||
QY 61 ITHFGPEANRLALSTPERINRDLWEGQREDLVR----- 96
Db |||||
QY 61 ITHFGPEANRLALSTPERINRDLWEGQREDLVR----- 96
Db |||||
QY 97 ---DPQSTYDYVRRKPRLMEDNRNARLGEVNSHRYTRLLLVKEHNSNPVQOQLDGT 153
Db |||||
QY 121 PRKDPQSTYDYVRRKPRLMEDNRNARLGEVNSHRYTRLLLVKEHNSNPVQOQLDGT 180
Db |||||
QY 154 RGHARTVGHQASPIKTIETLFEDEERPEPRTVVMQGAAGIGKSMIAHKWMDWADGKLF 213
Db |||||
QY 181 RGHARTVGHQASPIKTIETLFEDEERPEPRTVVMQGAAGIGKSMIAHKWMDWADGKLF 240
Db |||||
QY 214 QGRFDYLYFYNCREMNQSAECSDLI FSCWPEPSAPLOELIRVPERLLFIIDGFDL 273
Db |||||
QY 241 QGRFDYLYFYNCREMNQSAECSDLI FSCWPEPSAPLOELIRVPERLLFIIDGFDL 300
Db |||||
QY 274 PSFHDPOGWCLEWEKRPTELLNSLIRKLLPELSLITTRPTALEKHLRLEHPRHV 333
Db |||||
QY 301 PSFHDPOGWCLEWEKRPTELLNSLIRKLLPELSLITTRPTALEKHLRLEHPRHV 360
Db |||||
QY 334 EILGFSEAEKRYFYKFNHAEQAGVFNVRNEPLFTMCFVPLVWVCTCLOQQLG 393
Db |||||
QY 361 EILGFSEAEKRYFYKFNHAEQAGVFNVRNEPLFTMCFVPLVWVCTCLOQQLG 420
Db |||||
QY 394 GGLLRQTSRTTTAVYMLYLLSLMQPKGAPRLQPPNORGICSLAAGLWQKILFEQD 453
Db |||||
QY 421 GGLLRQTSRTTTAVYMLYLLSLMQPKGAPRLQPPNORGICSLAAGLWQKILFEQD 480
Db |||||
QY 454 LRKHGLDGEDVSAFLNMNIFQKDINCERYYSFIHLSFOEFAAAYIILDEGEAGAGPQD 513
Db |||||
QY 481 LRKHGLDGEDVSAFLNMNIFQKDINCERYYSFIHLSFOEFAAAYIILDEGEAGAGPQD 540
Db |||||
QY 514 VTRLLITEYAFSERSFLALTSRFLGGLNEETRSHLEKSLCWKVSPIHMDLQWTSQAQ 573
Db |||||
QY 541 VTRLLITEYAFSERSFLALTSRFLGGLNEETRSHLEKSLCWKVSPIHMDLQWTSQAQ 600
Db |||||
QY 574 SDGSTLQOQSLFFSCLYEIQEEBFQOALSHFOVIVVSNIAKMEHVMVSFCLKRCRCSA 633
Db |||||
QY 601 SDGSTLQOQSLFFSCLYEIQEEBFQOALSHFOVIVVSNIAKMEHVMVSFCLKRCRCSA 660
Db |||||
QY 634 QVLLHYGATYSADGEDRARCAGATLVLQRLPERTVLLDAYSEHLAAALCTNPNIELS 693
Db |||||
QY 661 QVLLHYGATYSADGEDRARCAGATLVLQRLPERTVLLDAYSEHLAAALCTNPNIELS 720
Db |||||
QY 694 LYRNALSGRGVKKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKLITRMDLSG 753
Db |||||
QY 721 LYRNALSGRGVKKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKLITRMDLSG 780
Db |||||

QY 934 LLAEGLOHPACRLQKWLWDSCLGTAKACENLYFTLGINQTLTDLTLNNALGDTGVRLLC 993
 |||||
 Db 961 LLAEGLOHPACRLQKWLWDSCLGTAKACENLYFTLGINQTLTDLTLNNALGDTGVRLLC 997
 |||||

QY 994 KRLSHPGCKLRVLMFGMDLNKMTSHSLAALRVTKPYLDIGC 1035
 |||||
 Db 978 -----WLFMGMDLNKMTSHSLAALRVTKPYLDIGC 1006
 |||||

RESULT 9

ADM04476

ID ADM04476 standard; protein; 1004 AA.

XX

AC ADM04476;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human protein of the invention SEQ ID NO:3161.

XX

KW human; gene therapy; diagnostic marker; pharmaceutical.

XX

OS Homo sapiens.

XX

PN EPI347046-A1.

XX

PD 24-SEP-2003.

XX

PF 12-APR-2002; 2002EP-00008400.

XX

PR 22-MAR-2002; 2002JP-00137785.

XX

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX

PI Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

XX

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX

DR WPI; 2003-723558/69.

XX

DR N-PSDB; ADM02033.

XX

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

XX

PS Claim 1; SEQ ID NO 3161; 305pp; English.

XX

CC The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a

CC protein sequence of the invention.

XX

SQ Sequence 1004 AA;

XX

Query Match 92.8%; Score 5077.5; DB 7; Length 1004;
 Best Local Similarity 91.9%; Pred. No. 0;
 Matches 976; Conservative 0; Mismatches 1; Indels 85; Gaps 3;

QY 1 MLRTAGRDGLCRSLTYLEELBAVELKKFKLVLTATLGECKIPWGSWEKAGPLEMAQLL 60

Db 1 MLRTAGRDGLCRSLTYLEELBAVELKKFKLVLTATLGECKIPWGSWEKAGPLEMAQLL 60

QY 61 ITHFGPEAWRLALSTFERINRKDLWEGQREDLVRLV----- 96

Db 61 ITHFGPEAWRLALSTFERINRKDLWEGQREDLVRLV----- 120

QY 97 ---DPQETRYDYVRKFLMEDNRVARGECVNLSHRYTRLLLVKHSNPMQVQOQLDGT 153

XX |||||

Db 121 PRKDPQETRYDYVRKFLMEDNRVARGECVNLSHRYTRLLLVKHSNPMQVQOQLDGT 180
 QY 154 RGHARTVGHQASPIKIEITLPEPDERPEPRTVVMQGAAGICKSMIAHKVMDWADGKLF 213
 |||||
 Db 181 RGHARTVGHQASPIKIEITLPEPDERPEPRTVVMQGAAGICKSMIAHKVMDWADGKLF 240
 |||||
 QY 214 QGRFDYLYINCREMNSQATSCSMQDLIFSCWPSPSAPLOELIRVPERLLFIIDGFDL 273
 |||||
 Db 241 QGRFDYLYINCREMNSQATSCSMQDLIFSCWPSPSAPLOELIRVPERLLFIIDGFDL 300
 |||||
 QY 274 PSFHDPOGWCLEWEKRPTELLNSLRKLLPELSLITTRTALEKLRHLEHPRHV 333
 |||||
 Db 301 PSFHDPOGWCLEWEKRPTELLNSLRKLLPELSLITTRTALEKLRHLEHPRHV 360
 |||||
 QY 334 EILGFSEAEKKEYFYKYFHNAEQAGQVFNVRDNEPLFTMCVFVLCVWVCTCQQOLEG 393
 |||||
 Db 361 EILGFSEAEKKEYFYKYFHNAEQAGQVFNVRDNEPLFTMCVFVLCVWVCTCQQOLEG 420
 |||||
 QY 394 GGLLRQTSRTTAVYMLYLLSLMQPKPGAPRLQPPNQRGLCSLAADGLWNQKILFBEQ 453
 |||||
 Db 421 GGLLRQTSRTTAVYMLYLLSLMQPKPGAPRLQPPNQRGLCSLAADGLWNQKILFBEQ 480
 |||||
 QY 454 LRKHGLDGEDVSAPLANNI FQKQINCERYYSFTHLSQEPFAAMYIILDEGEGAGDQD 513
 |||||
 Db 481 LRKHGLDGEDVSAPLANNI FQKQINCERYYSFTHLSQEPFAAMYIILDEGEGAGDQD 540
 |||||
 QY 514 VTRLLTEYAFSERSFLALTSRFLGGLNEETRSLSKSLCKWSPHMKMDLLOWIQSKAQ 573
 |||||
 Db 541 VTRLLTEYAFSERSFLALTSRFLGGLNEETRSLSKSLCKWSPHMKMDLLOWIQSKAQ 600
 |||||
 QY 574 SDGSTLQOQSLEFPFSCLYEIQEEFIQOALSHEQVIVVSNIASKMEHVSFCLKRCRSA 633
 |||||
 Db 601 SDGSTLQOQSLEFPFSCLYEIQEEFIQOALSHEQVIVVSNIASKMEHVSFCLKRCRSA 660
 |||||
 QY 634 QVHLHYGATYSADGEDRARCAGAHLLVQL-PERTVLLDAYSHSLAAALCTNPNLIELS 693
 |||||
 Db 661 QVHLHYGATYSADGEDRARCAGAHLLVQL-PERTVLLDAYSHSLAAALCTNPNLIELS 719
 |||||
 QY 694 LYRNALGSRGVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 753
 |||||
 Db 720 LYRNALGSRGVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 779
 |||||
 QY 754 NGVGFPGMMLLCEGLRHPQCRLOMIQLRKQLESGACQEMASVLGTNPHLVELDLTGNAL 813
 |||||
 Db 780 NGVGFPGMMLLCEGLRHPQCRLOMIQLRKQLESGACQEMASVLGTNPHLVELDLTGNAL 839
 |||||
 QY 814 EDIGLRLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 873
 |||||
 Db 840 EDIGLRLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 899
 |||||
 QY 874 GVLLLCBGLRHPCKLQTLRLGICRLGSAACEGLSVVLQANHNLRELDLSFNDLGDWGLW 933
 |||||
 Db 900 GVLLLCBGLRHPCKLQTLRL- - - - - 919
 |||||
 QY 934 LLAEGLOHPACRLQKWLWDSCLGTAKACENLYFTLGINQTLTDLTLNNALGDTGVRLLC 993
 |||||
 Db 961 KRLSHPGCKLRVLMFGMDLNKMTSHSLAALRVTKPYLDIGC 1004
 |||||

RESULT 10

ADP47728

ID ADP47728 standard; protein; 950 AA.

XX

AC ADP47728;

XX

DT 12-AUG-2004 (first entry)

XX

DE Human Monarch-1 (CATERPILLER 19.3) isoform III protein.

XX

KW Monarch-1; CATERPILLER 11.2; caspase recruitment domain;
KW CARD, transcription enhancer, R-binding, pyrin, lots of leucine repeat;
KW CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIASI;
KW cold-induced autoinflammatory syndrome 1; antiinflammatory; cytostatic;
KW inflammatory disease; cancer; gene therapy; human; purine;
KW CATERPILLER 19.3; chromosome 19q13; multiple sclerosis; isoform III.
XX Homo sapiens.
XX WO2004034093-A2.
XX 22-APR-2004.
XX 30-APR-2003; 2003WO-US013562.
XX 30-APR-2002; 2002US-0376626P.
XX (UYNC-) UNIV NORTH CAROLINA.
XX Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'Connor W;
XX Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;
XX WPI; 2004-348215/32.
XX N-PSDB; ADP47727.
XX New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3,
XX CATERPILLER 16.1, CATERPILLER 16.2 or CIASI polypeptide, useful in
XX preparing a composition for treating inflammatory disease or cancer.
XX Claim 18; SEQ ID NO 6; 205pp; English.
XX The invention relates to a novel isolated nucleic acid encoding a Monarch
XX -1, CATERPILLER (CARD [caspase recruitment domain], transcription
XX enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2,
XX CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIASI (cold-
XX induced autoinflammatory syndrome 1) polypeptide comprising the amino
XX acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or
XX its fragment. The nucleic acid of the invention demonstrates
XX antiinflammatory and cytostatic activities and may be useful in preparing
XX a composition for treating an inflammatory disease or cancer, possibly
XX via gene therapy. The current sequence is that of the human Monarch-1
XX (CATERPILLER 19.3) isoform III protein of the invention which is encoded
XX by DNA located on chromosome 19q13, in the multiple sclerosis
XX susceptibility region.
XX SQ Sequence 950 AA;
Query Match 87.7%; Score 4799.5; DB 8; Length 950;
Best Local Similarity 86.9%; Pred. No. 0;
Matches 923; Conservative 0; Mismatches 0; Indels 139; Gaps 2;
QY 1 MLRTAGDGLCRSLTYLEBAVELKKFKLYLGTATLGEGLKIPWGSMEKAGPLEMAQLL 60
Db 1 MLRTAGDGLCRSLTYLEBAVELKKFKLYLGTATLGEGLKIPWGSMEKAGPLEMAQLL 60
QY 61 ITHGPEAWRLALSTFERINRKNLWERGQEDLVR----- 96
Db 61 ITHGPEAWRLALSTFERINRKNLWERGQEDLVRTPPGPSSLGNQSTCLLEVLVT 120
QY 97 ---DPQETRYDYVRKFRMEDNARLGEVNLGSHRYTRLLLVKHEHNPVQVQQLDGT 153
Db 121 PRKDPQETRYDYVRKFRMEDNARLGEVNLGSHRYTRLLLVKHEHNPVQVQQLDGT 180
QY 154 RGHARTVGHQASPIKIEITLFPEDERPEPPRTVMQAGIGKSLAHKVMLDWADGKLF 213
Db 181 RGHARTVGHQASPIKIEITLFPEDERPEPPRTVMQAGIGKSLAHKVMLDWADGKLF 240
QY 214 QRFDFYLFVINCENMNQATSCMODLIFSCWPESAPLOELIRVPERLLFIIDGDELK 273
Db 241 QRFDFYLFVINCENMNQATSCMODLIFSCWPESAPLOELIRVPERLLFIIDGDELK 300
QY 274 PSFHDPPQGWCLWEKRPTELLNSLRKKLLPELSLLITRPTALEKHLRLEHPRHV 333

Db 301 PSFHDPPQGWCLWEKRPTELLNSLRKKLLPELSLLITRPTALEKHLRLEHPRHV 360
QY 334 EILGFSAEARKEYFKYFHNAEQAGOVNVRDNEPLFTMCVFPLVCWVCTCQQOQLG 393
Db 361 EILGFSAEARKEYFKYFHNAEQAGOVNVRDNEPLFTMCVFPLVCWVCTCQQOQLG 420
QY 394 GGLLRQTSRTTAVVYMLYLLSMQPKGAPRLQPPNQRGLCSLAADGLMNKILFEBQD 453
Db 421 GGLLRQTSRTTAVVYMLYLLSMQPKGAPRLQPPNQRGLCSLAADGLMNKILFEBQD 480
QY 454 LRKHGLDGEDVSFLNNMIFOKDINERYYSFIHLSFOEFFAAMYIILDEGGAGPDOD 513
Db 481 LRKHGLDGEDVSFLNNMIFOKDINERYYSFIHLSFOEFFAAMYIILDEGGAGPDOD 540
QY 514 VTRLITEYAFSPERSFLALTSRFLPGLLNEETRSHLEKSLCWKVPSPHFKMDLLQWISKAQ 573
Db 541 VTRLITEYAFSPERSFLALTSRFLPGLLNEETRSHLEKSLCWKVPSPHFKMDLLQWISKAQ 600
QY 574 SDGSTLQOQSLEFFSCLYEIQEEFIQALSHFQVIVVSNIAASKMEHVMVSFCLKRCRSA 633
Db 601 SDGSTLQOQSLEFFSCLYEIQEEFIQALSHFQVIVVSNIAASKMEHVMVSFCLKRCRSA 660
QY 634 QVHLHYGATYSADGEDRARCAGAHITLVQLRPRTVLLDAYSEHLAALCTNPNLIELS 693
Db 661 QVHLHYGATYSADGEDRARCAGAHITLVQLRPRTVLLDAYSEHLAALCTNPNLIELS 720
QY 694 LYRNALGSRGVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 753
Db 721 LYRNALGSRGVKLLCOGLRHPNCKLQNLRLKRCRISSACEDLSAALIANKNLTRMDLSG 780
QY 754 NGVFPFWMMLCEGLRHPQCRLOMTQLRKCOLESGACQEMASVLGTNPHLVLDLTGNAL 813
Db 781 NGVFPFWMMLCEGLRHPQCRLOMTQLRKCOLESGACQEMASVLGTNPHLVLDLTGNAL 840
QY 814 EDLGLRLCOGLRHPVCRRLTLWLKICRLTAACDELASTLSVNSQSLRELDLSNELGDL 873
Db 841 EDLGLRLCOGLRHPVCRRLTLWL----- 863
QY 874 GVLLLCLEGLRHPTCKLQTLRLGICRLGSAACEGLSVLQANHLRELDLSFNDLGDWGLW 933
Db 864 ----- 863
QY 934 LLAEGLOHPACRLQKLDSCGLTAKACENLYFTLGINQTLTDLYLTNNALGDTGVRLIC 993
Db 864 -----LWLDSCGLTAKACENLYFTLGINQTLTDLYLTNNALGDTGVRLIC 908
QY 994 KRLSHPGCKLRVLWLFGLMDLNKMTSHRLAALRVTKPYLDIGC 1035
Db 909 KRLSHPGCKLRVLWLFGLMDLNKMTSHRLAALRVTKPYLDIGC 950
RESULT 11
ADC31287
ID ADC31287 standard; protein; 865 AA.
XX
AC ADC31287;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human novel polypeptide sequence, SEQ ID NO:1369.
XX
XX Human; diagnostic; drug screening; forensics; gene mapping;
XX biodiversity assessment; Parkinson's disease; Alzheimer's disease;
XX neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
XX ulcers; osteoporosis; autoimmune disease; cancer;
XX molecular weight marker; food supplement; antiparkinsonian; nootropic;
XX neuroprotective; antianemic; anticoagulant; thrombolytic; vulnery;
XX antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
XX gene therapy; chromosome 19.
XX Homo sapiens.
XX WO2003029271-A2.
PN

XX 10-APR-2003.
PD 24-SEP-2002; 2002WO-US030474.
XX 24-SEP-2001; 2001US-0324631P.
XX (HYSE-) HYSEQ INC.
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Dmanac RT;
XX WPI; 2003-371981/35.
DR N-ESDB; ADC30316.
XX New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX Claim 20; SEQ ID NO 1369; 1185pp; English.
XX The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human polypeptide sequence of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 865 AA;
Query Match 82.6%; Score 4520; DB 7; Length 865;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 865; Conservative 0; Mismatches 0; Indels 58; Gaps 2;
QY 113 MEDNARLGEVNLSHRYTRLLLVKHSNPMQVQQLDTRGHARTVGHQAPKIKETL 172
DB 1 MEDNARLGEVNLSHRYTRLLLVKHSNPMQVQQLDTRGHARTVGHQAPKIKETL 60
QY 173 FEPDEERPEPRTVMQGAIGKSLAHKVMLDWADKGLFQGRFDYLFYINCREMNQSA 232
DB 61 FEPDEERPEPRTVMQGAIGKSLAHKVMLDWADKGLFQGRFDYLFYINCREMNQSA 120
QY 233 TECSMDLIIFSCWPEPSAPLQELIRVPERLLFIIDGFDLKPSPHDPQGPWCLCWEKRP 292
DB 121 TECSMDLIIFSCWPEPSAPLQELIRVPERLLFIIDGFDLKPSPHDPQGPWCLCWEKRP 180

QY 293 TELLNSLIRKKLLPELSLLITRPTALEKHLRLEHPRHVEILGFSEAEKKEYFYK 352
DB 181 TELLNSLIRKKLLPELSLLITRPTALEKHLRLEHPRHVEILGFSEAEKKEYFYK 240
QY 353 NAEQAGQVFNVRDNEPLFTMCFVPLVCWVCTCLOQLEGGLLROTSRTTTAVMYL 412
DB 241 NAEQAGQVFNVRDNEPLFTMCFVPLVCWVCTCLOQLEGGLLROTSRTTTAVMYL 300
QY 413 LSLMOPKPGAPRLQPPNQRLGLSLAAGLWNOKILFEODLRKHGIDGDEVSAFLN 472
DB 301 LSLMOPKPGAPRLQPPNQRLGLSLAAGLWNOKILFEODLRKHGIDGDEVSAFLN 360
QY 473 FQKDINCERYYSFIHLSFQEFFAAMYIYLDDEGGAGPDQDVTRLLTEYAFSERSFL 532
DB 361 FQKDINCERYYSFIHLSFQEFFAAMYIYLDDEGGAGPDQDVTRLLTEYAFSERSFL 420
QY 533 SRFLFGLNNEETSHLEKSLCWKVSPIHMDLLOWIOSKQSDGSTLQOGLSLEPFC 592
DB 421 SRFLFGLNNEETSHLEKSLCWKVSPIHMDLLOWIOSKQSDGSTLQOGLSLEPFC 480
QY 593 IOEEFTQOALSHFQVIVVSNIAKMEHMYSSFCLEKCRSAQVILHLYGATYSADGE 652
DB 481 IOEEFTQOALSHFQVIVVSNIAKMEHMYSSFCLEKCRSAQVILHLYGATYSADGE 540
QY 653 CSAGAHTLLVQLRPERTVLLDAYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCO 712
DB 541 CSAGAHTLLVQL-PERTVLLDAYSEHLAAALCTNPNIELSLYRNALGSRGVKLLCO 599
QY 713 HPNCKLQNLKRCRISSSACEDLSAALIANKNLTMDSLGNVGVPFGMMLLCGLRHP 772
DB 600 HPNCKLQNLKRCRISSSACEDLSAALIANKNLTMDSLGNVGVPFGMMLLCGLRHP 659
QY 773 CRLQMTOLRCKQESGACQESMAVILCTNPHLVELDTGNALDGLRLLCOGLRHPVC 832
DB 660 CRLQMTOLRCKQESGACQESMAVILCTNPHLVELDTGNALDGLRLLCOGLRHPVC 719
QY 833 RTLWLKICRTLTAACDELASTLSVNSQSLRELDLSLNEBGLDGLVLLLCGLRHPTCK 892
DB 720 RTLWLKICRTLTAACDELASTLSVNSQSLRELDLSLNEBGLDGLVLLLCGLRHPTCK 779
QY 893 RLGIICRIGSAACSEGLSVVLOANHNRLRELDLSFNDLGDWGLWLLAELQHPACRL 952
DB 780 R-----LD 782
QY 953 SCGLTAKACENLYFTIGINQTLTDLYLTNNALGDTGVRLCKLSHPGCKLVLMFGMD 1012
DB 783 SCGLTAKACENLYFTIGINQTLTDLYLTNNALGDTGVRLCKLSHPGCKLVLMFGMD 842
QY 1013 LNKWTHSRLLAALRVTKPYLDIGC 1035
DB 843 LNKWTHSRLLAALRVTKPYLDIGC 865
RESULT 12
ADP47730
ID ADP47730 standard; protein; 892 AA.
XX ADP47730;
AC ADP47730;
XX 12-AUG-2004 (first entry)
XX Human Monarch-1 (CATERPILLER 19.3) isoform IV protein.
XX Monarch-1; CATERPILLER 11.2; caspase recruitment domain;
KW CARD,transcription enhancer, R-binding, pyrin, lots of leucine repeat;
KW CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIASI;
KW cold-induced autoinflammatory syndrome 1; antiinflammatory; cytostatic;
KW inflammatory disease; cancer; gene therapy; human; purine;
KW CATERPILLER 19.3; chromosome 19q13; multiple sclerosis; isoform IV.
XX Homo sapiens.
OS
XX

SQ Sequence 635 AA;
Query Match 61.5%; Score 3364; DB 8; Length 635;
Best Local Similarity 100.0%; Pred. No. 8.1e-313;
Matches 635; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRTAGDGLCRSLTYLEELAEVLEKFKLYLTATLGEKIPWGSMEKAGPLEMAQLL 60
DB 1 MLRTAGDGLCRSLTYLEELAEVLEKFKLYLTATLGEKIPWGSMEKAGPLEMAQLL 60
QY 61 ITHFGPEAWRLALSTPERINRKLWERGQRELDVRDPQETDYVRRKFRMEDNARL 120
DB 61 ITHFGPEAWRLALSTPERINRKLWERGQRELDVRDPQETDYVRRKFRMEDNARL 120
QY 121 GECVNLSHRYTRLLVKEHNPVQVQQLDTRGHARTVGHQASPIKTIETLPEPDEEP 180
DB 121 GECVNLSHRYTRLLVKEHNPVQVQQLDTRGHARTVGHQASPIKTIETLPEPDEEP 180
QY 181 EPRTVVMQGAAGIGKSMIAHKVMDWADGKLFQGRFDYLYINCREMNQSAATECSMDL 240
DB 181 EPRTVVMQGAAGIGKSMIAHKVMDWADGKLFQGRFDYLYINCREMNQSAATECSMDL 240
QY 241 IFSCWPPSAPLOELIRVPERLLFIIDGFDLKPSPHDPQGPWCLCWEKKRPTTELLNSL 300
DB 241 IFSCWPPSAPLOELIRVPERLLFIIDGFDLKPSPHDPQGPWCLCWEKKRPTTELLNSL 300
QY 301 IRKLLPELSLITTRPTALEKHLRLLEHPRHVEILGFSEARKEYFYKVFHNAEQAGV 360
DB 301 IRKLLPELSLITTRPTALEKHLRLLEHPRHVEILGFSEARKEYFYKVFHNAEQAGV 360
QY 361 FNYVRDNEPLFTMCVFLVCMVCTCLQQLEGGLRLQTSRTTAVMYLYLSLMQPKP 420
DB 361 FNYVRDNEPLFTMCVFLVCMVCTCLQQLEGGLRLQTSRTTAVMYLYLSLMQPKP 420
QY 421 GAPLQPPNQRGLCSLAADGLMNQKILFEEODLRKGLDGEDVSAFLNWNIFQKDNCE 480
DB 421 GAPLQPPNQRGLCSLAADGLMNQKILFEEODLRKGLDGEDVSAFLNWNIFQKDNCE 480
QY 481 RYYSFIHLSFOEFPAAMYILDEEGGAGPDQDVTRLLTYATRSERFLALTSRFLFGLL 540
DB 481 RYYSFIHLSFOEFPAAMYILDEEGGAGPDQDVTRLLTYATRSERFLALTSRFLFGLL 540
QY 541 NEETRSHLEKSLCWKSPHIMDLOWIQSAQSDGSTLQGSLEFFSCLYEIQEEFFIQ 600
DB 541 NEETRSHLEKSLCWKSPHIMDLOWIQSAQSDGSTLQGSLEFFSCLYEIQEEFFIQ 600
QY 601 QALSHFQVIVVSNIAASKMEHVMVSSFCILKCRSAQV 635
DB 601 QALSHFQVIVVSNIAASKMEHVMVSSFCILKCRSAQV 635

RESULT 15
ID ADE36457
XX ADE36457 standard; protein; 603 AA.
AC ADE36457;
XX ADE36457;
XX 29-JAN-2004 (first entry)
XX Human PAN6 leucine-rich-repeat domain (LLR) seq id 64.
DE cystostatic; immunosuppressive; vulnary; antiinflammatory; vasotropic;
KW anti-allergic; antiulcer; dermatological; cerebroprotective; cardiac;
KW antiparkinsonian; nootropic; neuroprotective; anti-HIV; gene therapy;
KW NF-kappaB activation inhibitor; PAAD domain containing polypeptide;
KW PAAD and nucleotide binding protein 2-6; PAN 2-6; pyrin 2;
KW apoptosis-associated speck-like protein; caspase recruitment domain 2;
KW ASC-2; nuclear factor kappa B activation inhibitor; NB-ARC domain;
KW apoptosis; NF-kappaB induction; cytokine processing;
KW cytokine receptor signaling caspase-mediated proteolysis;
KW c-Jun N-terminal kinase activation; cell life; cell death; apoptosis;
KW inflammation; cell adhesion; cancer; keratinocyte; hyperplasia;
KW neoplasia; keloid benign prostatic hypertrophy; inflammatory hyperplasia;

KW fibrosis; smooth muscle cell proliferation; balloon angioplasty;
KW restenosis; leukaemia; lymphoma; inflammatory disease; allergy;
KW arthritis; lupus; schrojen's syndrome; Crohn's disease;
KW ulcerative colitis; graft versus host disease; stroke; heart failure;
KW neurodegenerative disease; parkinson's disease; Alzheimer's disease; HIV;
KW cancer therapy; PAAD domain family; human; PAN6; leucine-rich-repeat;
LLR.
XX Homo sapiens.
XX US2003077699-A1.
PN 24-APR-2003.
XX 25-SEP-2001; 2001US-00965621.
XX 26-SEP-2000; 2000US-00671760.
PR 26-SEP-2000; 2000US-0367367P.
XX (REED/) REED J C.
PA (GODZ/) GODZIK A.
PA (CHUZ/) CHU Z.
PA (PAWL/) PAWLOWSKI K.
PA (FIOR/) FIORENTINO L.
PA (ARIZ/) ARIZA M E.
PA (STEHL/) STEHLIK C.
XX Reed JC, Godzik A, Chu Z, Pawlowski K, Fiorentino L, Ariza ME;
PI Stehlik C;
XX WPI; 2002-471256/50.
XX Novel isolated PAAD domain containing polypeptide useful for inducing
PT apoptosis by inhibiting nuclear factor kappa B activation and in gene
PT therapy for treating cancer.
XX Claim 24; SEQ ID NO 64; 93pp; English.
XX The invention describes an isolated PAAD domain containing polypeptide
CC (I) comprising 80% identity to the amino acid sequence of PAAD and
CC nucleotide binding protein (PAN) 2-6, pyrin 2, apoptosis-associated speck
CC -like protein containing a caspase recruitment domain (ASC)-2 fully
CC defined in specification, where (I) is biologically active. (I) is useful
CC for identifying a (I)-associated polypeptide, an agent altering that
CC association and agents that modulate PAAD domain mediated inhibition of
CC nuclear factor kappa B (NF-kappaB). A NB-ARC domain polypeptide is useful
CC for identifying an agent that modulates the activity of the NB-ARC domain
CC of (I). (I) or its functional fragments is useful in altering cellular or
CC biochemical process such as apoptosis, NF-kappaB induction, cytokine
CC processing, cytokine receptor signaling caspase-mediated proteolysis or c
CC -Jun N-terminal kinase activation, thus having modulating effect on cell
CC life and death (apoptosis) inflammation, cell adhesion or other cellular
CC or biochemical processes. (I) is useful for treating cancer pathologies,
CC keratinocyte, hyperplasia, neoplasia, keloid benign prostatic
CC hypertrophy, inflammatory hyperplasia, fibrosis, smooth muscle cell
CC proliferation in arteries following balloon angioplasty (restenosis),
CC leukaemia, lymphomas; inflammatory diseases such as allergies, arthritis,
CC lupus, schrojen's syndrome, Crohn's disease and ulcerative colitis, graft
CC versus host disease, stroke, heart failure, neurodegenerative diseases
CC such as parkinson's and Alzheimer's disease, human immunodeficiency virus
CC infection (HIV). (I) is useful for diagnosing cancer or monitoring cancer
CC therapy. This is the amino acid sequence of a human PAAD and nucleotide
CC binding protein PAN6 leucine-rich-repeat domain (LLR).
XX Sequence 603 AA;

Query Match 57.8%; Score 3163; DB 5; Length 603;
Best Local Similarity 100.0%; Pred. No. 1.4e-293;
Matches 603; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 429 PNQRGLCSLAADGLMNQKILFEEODLRKGLDGEDVSAFLNWNIFQKDNCEYYSFIHL 488
DB 1 PNQRGLCSLAADGLMNQKILFEEODLRKGLDGEDVSAFLNWNIFQKDNCEYYSFIHL 60

[illegible]

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Job time : 180 secs

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